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(12) **United States Patent**
Bowen et al.(10) **Patent No.:** US 9,328,356 B2
(45) **Date of Patent:** May 3, 2016(54) **PESTICIDAL NUCLEIC ACIDS AND PROTEINS AND USES THEREOF**(75) Inventors: **David J. Bowen**, Glencoe, MO (US); **Gregory J. Bunkers**, Wildwood, MO (US); **Catherine Chay**, Ballwin, MO (US); **John W. Pitkin**, Wildwood, MO (US); **Timothy J. Rydel**, St. Charles, MO (US); **Eric J. Sturman**, Wildwood, MO (US); **Uma R. Sukuru**, Chesterfield, MO (US); **Brook Van Scyoc**, St. Louis, MO (US); **Stanislaw Flasinski**, St. Louis, MO (US)(73) Assignee: **Monsanto Technology LLC**, St. Louis, MO (US)

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C07K 14/325 (2006.01)
A01N 63/02 (2006.01)(52) **U.S. Cl.**CPC *C12N 15/8285* (2013.01); *A01N 63/02* (2013.01); *C07K 14/325* (2013.01); *C12N 15/8286* (2013.01)(58) **Field of Classification Search**

None

See application file for complete search history.

(56)

References Cited

U.S. PATENT DOCUMENTS

5,770,431 A *	6/1998	Liu et al.	435/252.3
6,028,246 A *	2/2000	Lambert et al.	800/279
6,063,756 A	5/2000	Donovan et al.	
2003/0049243 A1	3/2003	Liu et al.	
2003/0144192 A1	7/2003	Donovan et al.	
2006/0191034 A1	8/2006	Baum et al.	

FOREIGN PATENT DOCUMENTS

WO 9408010 A1 4/1994

OTHER PUBLICATIONS

Argôlo-Filho et al, 2014, Insects 5:62-91.*

Guo et al (2004, Proc. Natl. Acad. Sci. USA 101: 9205-9210).*
Böckenhoff et al., "Studies on the Nutrient Uptake by the Beet Cyst Nematode Heterodera schachtii by in situ Microinjection of Fluorescent Probes into the Feeding Structures in Arabidopsis thaliana", Parasitology, 1994, pp. 249-255, vol. 109, No. 2.

Urwin et al., "Resistance to Both Cyst and Root-Knot Nematodes Conferred by Transgenic Arabidopsis Expressing a Modified Plant Cystatin", The Plant Journal, 1997, pp. 455-461, vol. 12, No. 2.

* cited by examiner

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(57) **ABSTRACT**

The invention provides compositions comprising polynucleotide molecules encoding certain pesticidal polypeptides which exhibit plant parasitic nematode and/or insect control properties, and are particularly directed to controlling plant parasitic pest species of nematodes and insects known to infest crop plant species. Methods for controlling pests are disclosed in which the toxic proteins are provided in the diet of the targeted plant pests. The invention also provides compositions such as nucleic acids, proteins, and plant and bacterial cells, plants, and seeds containing the nucleic acid and protein compositions, as well as methods and kits for identifying, detecting, and isolating the compositions of the present invention. The invention further provides a method of producing crops from recombinant seeds which contain the polynucleotide molecules encoding the pesticidal polypeptides of the present invention.

15 Claims, No Drawings

1**PESTICIDAL NUCLEIC ACIDS AND PROTEINS AND USES THEREOF****CROSS REFERENCE TO RELATED APPLICATIONS**

This application claims priority to U.S. Provisional Application Ser. No. 61/441,697 and U.S. Provisional Application Ser. No. 61/441,709, both filed Feb. 11, 2011, which are incorporated herein by reference.

INCORPORATION OF SEQUENCE LISTING

The Sequence Listing accompanying this application is contained within the computer readable file "38-21(57560) SEQUENCE LISTING_ST25.txt" submitted electronically and contemporaneously with the filing of this application through the USPTO EFS-Web. The file is 105 kilobytes (measured in MS-Windows), was created on 19 Jan. 2012, and is incorporated herein by reference.

FIELD OF THE INVENTION

The invention relates to novel polynucleotide and protein compositions that, when expressed and/or produced in plants, impart resistance to plant pathogenic nematodes and insect infestation. The polynucleotides and proteins can be expressed in plant and bacterial cells, and the plant cells can be regenerated into transgenic (recombinant) plants, plant tissues, plant parts, and seeds. Compositions derived from such plants, plant materials, and seed that contain detectable amounts of such polynucleotides and proteins are included within the scope of the invention. The invention also relates to compositions and methods for controlling plant pathogenic nematodes and insect pests of crop plants.

BACKGROUND OF THE INVENTION

The increasing human population will require higher yields of food, feed, and fiber from crop plants on decreasing amounts of arable land. Several types of insects and nematodes are known to reduce yield of crops produced from plants. Plant pests damage plant parts, including roots, developing flower buds, flowers, leaves, stems, and seeds, which leads to lower yields.

Traditional approaches for controlling plant pests have used chemical control agents and construction of inter-specific hybrids between crops and their wild-type relatives as sources of resistant germplasm. Chemical pest control agents, although effective, have several disadvantages. Many chemical control agents are expensive to manufacture, and are characterized as pollutants because they persist in the environment as a result of their resistance to microbial degradation. Chemical control agents require on-farm formulation, which increases the safety risk to the farmer due to the exposure to chemical agent formulations. The chemical agent formulations have to be applied at least once and often, more than once per growing season, increasing the carbon footprint related to these compositions. Methods and compositions employing plant biotechnology pest control agents are also effective means for controlling plant pests, for instance through plant expression of one or more pest control agents that are generally selectively toxic to a particular target pest when ingested by the pest. Unlike chemical agents, biotech approaches have been demonstrated to be environmentally friendly, have no known safety risks when used by farmers, and are economical in terms of carbon footprint impact and

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ease of use for deployment by the farmer. However, there are only a few examples of such biotech compositions and methods for controlling such pests, and even fewer if any examples of any biotechnology approaches that have demonstrated efficacy in controlling plant pathogenic nematodes. Thus, there is a need for new compositions and methods for protecting plants from such pest infestation, generally for the purpose of maintaining and enhancing yields of crops produced from such plants, and for sustaining and providing food, feed and fiber for the increasing human population.

SUMMARY OF THE INVENTION

15 Polynucleotide molecules are provided encoding exemplary pesticidal polypeptides as set forth in SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:46, SEQ ID NO:50, SEQ ID NO:54, SEQ ID NO:58, and SEQ ID NO:60. Polypeptides having an amino acid sequence exhibiting from at least about 45% to about 99.9% identity to the pesticidal protein (polypeptide) sequences as set forth in any of the foregoing protein sequences (any percentage in between 45 and 99.9) and exhibiting substantially equivalent (biologically functional equivalent) pesticidal activity as any one of these sequences are specifically contemplated. Fragments of these polypeptide sequences that exhibit the requisite pesticidal activity are intended to be within the scope of 20 the present invention. Such polynucleotides may be extracted and/or obtained directly from a host cell or made artificially through various means of synthesis, and in either case, are considered to be recombinant polynucleotides.

25 Polynucleotides containing one or more nucleotide sequence segments encoding the pesticidal proteins of the present invention are provided, which may be operably linked to a heterologous promoter that initiates expression of the sequence region in a designated host cell, resulting in the production or manufacture of the pesticidal protein in the host cell. The promoter may include a plant-expressible promoter, a promoter that functions in one or more species of bacteria, and a yeast functional promoter, or combinations thereof. The plant-expressible promoter may include any number of promoters known in the art, including but not limited to corn 30 sucrose synthetase 1 promoter, corn alcohol dehydrogenase 1 promoter, corn light harvesting complex promoter, corn heat shock protein promoter, pea small subunit RuBP carboxylase promoter, Ti plasmid mannopine synthase promoter, Ti plasmid nopaline synthase promoter, petunia chalcone isomerase promoter, bean glycine rich protein 1 promoter, Potato patatin promoter, lectin promoter, CaMV 35S promoter, FMV promoter, ubiquitin promoters promoter, and the S E9 small subunit RuBP carboxylase promoter.

35 Isolated polynucleotide segments are provided for use as probes and/or primers, which may be from about 20 to about 1000 contiguous nucleotides in length or any length in between twenty and one thousand contiguous nucleotides, and exhibit at least about 90% identity to the same contiguous length of nucleotides as set forth in any of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59,

SEQ ID NO:61, and SEQ ID NO:63, or the complement of any of the foregoing polynucleotide sequences.

In another aspect of the invention, polynucleotides encoding any of the pesticidal polypeptides set forth above are provided in recombinant expression cassettes. The expression cassettes can be provided in vectors for use in replicating, maintaining and transferring the nucleic acid component encoding the pesticidal proteins of the present invention. The vectors of the present invention contain at least a sequence region that encodes the polypeptide as set forth above. The vector includes a plasmid, baculovirus, artificial chromosome, virion, cosmid, phagemid, phage, or viral vector.

Host cells may be any appropriate transgenic host cell including but not limited to microbial cells (microorganisms) such as an *Agrobacterium*, a *Bacillus*, an *Escherichia*, a *Salmonella*, a *Pseudomonas*, a *Rhizobium* bacterial cell, a yeast cell such as a *pichia* yeast or *saccharomyces* species yeast cell, or a plant cell. Vectors as described above can be provided in a transgenic microbial host cell. The transgenic microbial host cell includes a prokaryotic or eukaryotic host cell. The transgenic prokaryotic host cell is a bacterial cell and the transgenic eukaryotic host cell is a plant or a fungal/yeast cell. The transgenic bacterial cell includes a recombinant bacterium including a *Bacillus thuringiensis*, *Bacillus subtilis*, *Bacillus megaterium*, *Bacillus cereus*, *Bacillus laterosporous*, *Escherichia*, *Salmonella*, *Agrobacterium*, *Rhizobium*, or *Pseudomonas* cell. The transgenic plant host cell includes a monocotyledonous or dicotyledonous plant cell and may include any plant cell from the Group of Plants or Plant Group set forth below. To the extent that a microbial cell is a plant cell, the cell can be obtained from any plant, plant tissue, plant part or seed from a plant selected from the group consisting of any of the following, including but not limited to barley, bean, broccoli, cabbage, canola (rapeseed), carrot, cassava, castor, cauliflower, celery, chickpea, Chinese cabbage, coffee, corn (including sweet corn), clover, cotton, a cucurbit, cucumber, deciduous trees (including but not limited to banana, citrus, eucalyptus, nut trees (including but not limited to hickory, pecan, and walnut trees), oak trees (including but not limited to live oak, pin oak, and post oak trees), olive, palm (including coconut palm), poplar, sweet gum, and rootstocks of all of the preceding trees), eggplant, evergreen trees (including but not limited to Douglas fir), flax, garlic, grape, grasses (including but not limited to alfalfa, pasture grass, switchgrass, and turf grass), hops, leek, lettuce, millets, melons (including but not limited to cantaloupe, honeydew melon, and watermelon), oat, onion, pea, peanut, pepper, pigeonpea, pine (including Loblolly pine, Radiata pine, and Southern pine), potato, pumpkin, radish, rice, rye, safflower, shrub, sorghum, soybean, spinach, squash, strawberry, sugar beet, sugarcane, sunflower, sweet corn, sweet potato, tea, tobacco, tomato, triticale, or wheat. The aforementioned are referenced herein as the "Group of Plants" or the "Plant Group".

Recombinant plants, plant tissue, plant parts, or seed contain the polynucleotides of the present invention and express the proteins of the present invention from such polynucleotides. The plant part is a leaf, a stem or a flower, a sepal, a fruit, a root, or a seed. Products produced from a recombinant plant of the present invention are also contemplated, and can include at least any of the following: oil, meal, lint and seed of the recombinant plant. The polynucleotides and proteins of the present invention are present in a detectable amount in the plants and plant products, and are useful at least as markers for tracking the presence of seeds and plant tissues containing

the polynucleotide and proteins through trade and commerce, in fields of crops, and in various embodiments referenced herein.

There is provided a method of detecting and/or isolating in or from a biological sample, a polynucleotide molecule encoding a pesticidal polypeptide of the present invention in which the steps of the method include (i) selecting a pair of oligonucleotide primers that produce an amplicon encoding all or a representative amount of the pesticidal polypeptide of the present invention when used together in an amplification reaction with the biological sample containing the polynucleotide; (ii) producing the amplicon from the polynucleotide; (iii) detecting and/or isolating the amplicon; and (iv) generating nucleotide sequence information corresponding to the amplicon to identify and confirm the presence (or absence) of a segment of a polynucleotide molecule encoding all or a representative amount of the pesticidal polypeptide. Alternatively, the detecting and/or isolating step can be conducted by providing a polynucleotide probe derived from a sufficient length of DNA or RNA encoding the pesticidal polypeptide that hybridizes under specific or under stringent hybridization conditions to such a polynucleotide encoding a pesticidal polypeptide of the present invention.

Methods of controlling or killing a target lepidopteran pest, coleopteran pest, or plant pathogenic nematode pest population are provided and include contacting the pest population with a pesticidally-effective amount of the polypeptide as set forth above. The "lepidopteran pest population" includes *Spodoptera frugiperda*, *Spodoptera exigua*, *Mamestra configurata*, *Agrotis ipsilon*, *Trichoplusia ni*, *Pseudeplusia includens*, *Anticarsia gemmatalis*, *Hypena scabra*, *Heliothis virescens*, *Agrotis subterranea*, *Pseudaletia unipuncta*, *Agrotis orthogonia*, *Ostrinia nubilalis*, *Amyelois transitella*, *Crambus caliginosellus*, *Herpetogramma licarsialis*, *Homoeosoma electellum*, *Elasmopalpus lignosellus*, *Cydia pomonella*, *Endopiza viteana*, *Grapholita molesta*, *Suleima helianthana*, *Plutella xylostella*, *Pectinophora gossypiella*, *Lymantria dispar*, *Blatta orientalis*, *Blatella asahinai*, *Blattella germanica*, *Supella longipalpa*, *Periplaneta americana*, *Periplaneta brunnea*, *Leucophaea maderae*, *Alabama argillacea*, *Archips argyrospila*, *A. rosana*, *Chilo suppressalis*, *Cnaphalocrocis medinalis*, *Crambus caliginosellus*, *C. teterrellus*, *Diatraea grandiosella*, *D. saccharalis*, *Earias insulana*, *E. vittella*, *Helicoverpa armigera*, *H. zea*, *Heliothis virescens*, *Herpetogramma licarsialis*, *Lobesia botrana*, *Pectinophora gossypiella*, *Phylloconistis citrella*, *Pieris brassicae*, *P. rapae*, *Plutella xylostella*, *Spodoptera exigua*, *S. litura*, *S. frugiperda*, *Tuta absoluta*. The "coleopteran pest population" includes *Anthonomus grandis*, *Lissorhoptrus oryzophilus*, *Sitophilus granaries*, *Sitophilus oryzae*, *Hypera punctata*, *Sphenophorus maidis*, *Leptinotarsa decemlineata*, *Diabrotica virgifera virgifera*, *Diabrotica barberi*, *Diabrotica undecimpunctata howardi*, *Chaetocnema pulicaria*, *Phyllotreta cruciferae*, *Colaspis brunnea*, *Oulema melanopus*, *Zygogramma exclamationis*, *Epilachna varivestis*, *Popillia japonica*, *Cyclocephala boreali*, *Cyclocephala immaculata*, *Rhizotrogus majalis*, *Phyllophaga crinita*, *Ligyrus gibbosus*, *Melanotus spp.*, *Conoderus spp.*, *Limonius spp.*, *Agriotes spp.*, *Cteniceridae spp.*, *Aeolus spp.*, *Eleodes spp.* The "plant pathogenic nematode population" includes *Heterodera glycines* (soybean cyst nematode), *Heterodera avenae*, *Globodera rostochiensis*, *Globodera pallida*, *Pratylenchus zeae* (a root knot nematode), *Meloidogyne javanica*, *Pratylenchus brachyurus* (a root knot nematode), *Meloidogyne hapla*, *Meloidogyne incognita*.

An alternative method for controlling such plant pest infection includes providing a pest inhibitory amount of a pesti-

cidal polypeptide of the present invention to a pest susceptible to the polypeptide, thereby controlling the pest. The pest is an insect or a nematode. The insect may be any insect within the taxonomical orders including Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthoptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, or Trichoptera (hereinafter, the "Insect Orders"). The nematode may be from any genus of nematodes referred to as *Acontylus*, *Anguina*, *Aorolaimus*, *Aphasmatylenchus*, *Aphelenchoides*, *Aphelenchus*, *Atalodera*, *Atylenchus*, *Bakerinema*, *Belonolaimus*, *Brachydorus*, *Bursaphelenchus*, *Cacopaurus*, *Caloosia*, *Carpodorus*, *Criconema*, *Criconemella*, *Cryphodera*, *Ditylenchus*, *Dolichodorus*, *Etylenchus*, *Globodera*, *Gracilaculus*, *Helicotylenchus*, *Hemicriconemoides*, *Hemicyclophora*, *Heterodera*, *Hirschmanniella*, *Histotylenchus*, *Hoplolaimus*, *Hoplotylus*, *Longidorus*, *Macrotrophurus*, *Meliododera*, *Meloidogyne*, *Merlinius*, *Morulaimus*, *Nacobbus*, *Nothanguina*, *Nothotylenchus*, *Paralongidorus*, *Paratrichodorus*, *Paratrophurus*, *Paratylenchus*, *Peltamigratus*, *Pratylenchoides*, *Pratylenchus*, *Psilenchus*, *Radopholoides*, *Radopholus*, *Rhadinaphelenchus*, *Rototylenchus*, *Rotylenchoides*, *Rotylenchus*, *Sarisodera*, *Scutellonema*, *Sphaeronema*, *Subanguina*, *Telotylenchoides*, *Telotylenchus*, *Trichotylenchus*, *Trophonema*, *Trophiylenctus*, *Trophurus*, *Tylenchorhynchus*, *Tylenchulus*, *Tylenchus*, *Tyloadorus*, *Xiphinema*, or *Zygotylenchus* (hereinafter, the "Nematode Species"). In related embodiments, the nematode species includes cyst and related nematodes such as *Heterodera glycines* (soybean cyst nematode), *Heterodera schachtii* (beet cyst nematode), *Heterodera avenae* (cereal cyst nematode), and *Globodera rostochiensis* and *Globodera pallida* (potato cyst nematodes), *Pratylenchus zeae*, *Meloidogyne javanica*, *Pratylenchus brachyurus*, *Meloidogyne hapla*, or *Meloidogyne incognita* (hereinafter, the "Cyst Nematode" group). The pest inhibitory amount of the pesticidal polypeptide is provided in the diet of the pest, and the diet of the pest can be a part of a recombinant plant, seed of such plant, or product of the plant. The pest inhibitory amount of the polypeptide may also be provided in a topical formulation to a plant. Such formulation could include a preparation containing bacterial cells, bacterial spores, and parasporal crystals which contain or are producing one or more of the polypeptides/toxic agents of the present invention in a sufficient amount to inhibit the pest infestation of the plant to which the formulation is applied. A formulation for controlling nematode or insect species within the scope of the present invention may consist of recombinant bacterial cells and/or spores which may be producing the toxic proteins of the present invention, or parasporal crystals that contain pesticidal amounts of the polypeptide. The bacterial cells, spores, or parasporal crystals are typically from *Bacillus* species. Antibodies are contemplated that specifically bind to a polypeptide having the amino acid sequence as set forth in any of SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:46, SEQ ID NO:50, SEQ ID NO:54, SEQ ID NO:58, and/or SEQ ID NO:60.

Such antibodies are useful at least in methods of detecting pesticidal polypeptides such as those set forth in SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID

NO:46, SEQ ID NO:50, SEQ ID NO:54, SEQ ID NO:58, and/or SEQ ID NO:60 in a biological sample. A method of detecting such proteins could include the steps of contacting the biological sample with an antibody that specifically binds to one or more of the proteins of the present invention, and detecting the binding of the antibody to the pesticidal polypeptide. Alternatively, proteins of the present invention, or proteins that are substantially related to the proteins of the present invention can be detected in or isolated from a biological sample either by directly identifying the protein in the sample using for example, antibodies as indicated above, or by screening for the presence of a polynucleotide encoding the pesticidal protein. Detecting the polynucleotide encoding such protein could include the steps of: i) selecting a pair of primers that produce an amplicon encoding the pesticidal protein when used together in an amplification reaction with the polynucleotide; ii) producing the amplicon by using the polynucleotide as a template in the amplification reaction; iii) detecting/isolating the amplicon; iv) generating DNA sequence information corresponding to the amplicon to confirm that the amplicon encodes the pesticidal protein; and v) testing the pesticidal protein to confirm pesticidal activity. Alternatively, a method for detecting the protein of the present invention, or a related pesticidal protein such as a δ-endotoxin polypeptide, in a biological sample could include the steps of: i) obtaining a biological sample suspected of containing a δ-endotoxin polypeptide; ii) contacting the sample with an antibody that specifically binds to the polypeptide under conditions effective to allow the formation of immune complexes; and iii) detecting the immune complexes so formed. Another alternative method for detecting a target pesticidal polypeptide of the present invention in a sample may include the steps of: i) contacting the sample with an antibody that specifically binds the target pesticidal polypeptide; ii) detecting the binding of the antibody to the target in the sample; and iii) identifying the target as a pesticidal polypeptide exhibiting at least 90% amino acid sequence identity to any one of the proteins set forth in SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:46, SEQ ID NO:50, SEQ ID NO:54, SEQ ID NO:58, and/or SEQ ID NO:60.

45 Detection methods can be conducted using reagents and instructions packaged together in kit form and are useful for detecting the proteins and polynucleotides of the present invention. Such kits could include a first reagent or antibody that binds specifically to the polypeptide, or specifically to a peptide or an epitope derived therefrom; and a second reagent such as a control polypeptide corresponding to any of the proteins as set forth in any of SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:46, SEQ ID NO:50, SEQ ID NO:54, SEQ ID NO:58, and/or SEQ ID NO:60, or a peptide, or an epitope derived therefrom.

50 In another aspect of the present invention, there is provided a method of preparing insect resistant plants. Such plants can be prepared by contacting a recipient plant cell with a transgene that encodes one or more of the polypeptides of the present invention under conditions permitting the uptake of the transgene by the cell, and selecting a recipient cell in which the transgene has been incorporated into the cell genome, and regenerating a plant from the selected recipient cell. The regenerated plant is confirmed to be a fertile transgenic plant exhibiting pest resistance, and the pest resistance includes resistance to plant pathogenic nematode infestation

and one other pest resistance selected from resistance against to a coleopteran insect or to a lepidopteran insect. The contacting step includes any one or ore of the methods known in the art, including microprojectile bombardment, electroporation or *Agrobacterium*-mediated plant cell transformation. The regenerated plant is resistant to at least one of the members of the plant parasitic nematode group including *Heterodera* species, *Globodera* species, *Meloidogyne* species, *Rotylenchulus* species, *Hoplolaimus* species, *Belonolaimus* species, *Pratylenchus* species, *Longidorus* species, *Paratrichodorus* species, *Ditylenchus* species, *Xiphinema* species, *Dolichodorus* species, *Helicotylenchus* species, *Radopholus* species, *Hirschmanniella* species, *Tylenchorhynchus* species, or *Trichodorus* species.

Transgenic seed containing one or more polynucleotide segments encoding one or more of the proteins of the present invention may be produced comprising the steps of: transforming a plant with a transgene that encodes the polypeptide as set forth above, the transgene operably linked to a promoter that expresses the transgene in a plant, thereby obtaining a fertile transgenic plant comprising the transgene; and growing the plant under appropriate conditions to produce the transgenic seed.

Progeny of any generation of a pest resistance-enhanced fertile transgenic plant can be produced from such transgenic plants and seeds of the foregoing plants and seed, wherein the progeny contain the polynucleotide and encode the protein(s) of the present invention, and has enhanced pest resistance against a coleopteran insect, lepidopteran insect, or a plant pathogenic nematode relative to the corresponding non-transgenic plant.

Pest resistant plants can be produced by following the method of: (a) crossing a pest resistant plant comprising a transgene that encodes the polypeptide as set forth above with another plant; (b) obtaining at least one progeny plant derived from the cross of (a); and (c) selecting progeny that comprises the transgene, wherein the progeny is resistant against a coleopteran insect, lepidopteran insect, or a plant pathogenic nematode.

Seed can be produced from the plants of the present invention. Seed containing a polynucleotide molecule encoding one or more of the proteins of the present invention, whether homozygous or heterozygous for the particular transgenic allele, can be packaged for planting in a field, and a crop can be produced from the planted seed. The crop from such plants can be harvested, and if seed of the harvested generation are the crop (such as soybean, rice, wheat, canola or corn and the like), at least 50% of the harvested crop are seed containing the polynucleotide molecule.

Commodity products (or biological samples) containing a plant or plant part as set forth above that can be shown to contain a detectable amount of a polypeptide having the amino acid sequence of any of the proteins of the present invention, or polynucleotides encoding any such protein. The detection of the polypeptide or the polynucleotide in the commodity (or biological sample) is determinative of the presence of the plant or plant part in the commodity (or biological sample), and all such commodity products in which the polypeptide is detectable to a level of at least about (i) one part per million, (ii) or one nanogram per gram fresh weight of tissue, are within the scope of the present invention. A plant cell of the present invention may be regenerated into a recombinant plant which can produce a plant part containing any of the proteins of the present invention. The plant part includes a leaf, a stem a flower, a sepal, a fruit, a root, or a seed. Products produced from a recombinant plant or plant part contain a detectable amount of any one of the proteins of

the present invention, or polynucleotide segments encoding such proteins. Such products include oil, meal, lint and seed of such recombinant plants. The detectable amount of the proteins and/or polynucleotides are useful as molecular markers for tracking and/or identifying the presence of seeds and plant tissues of the present invention as these are moved through commerce.

The proteins of the present invention originate from *Bacillus thuringiensis* species of bacteria, and as such, are likely to be characterized as delta-endotoxins, and are typically produced from a recombinant polynucleotide. Such delta endotoxin proteins will have an amino acid sequence that exhibits at least from about 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 99.9%, or 100% amino acid sequence identity to the amino acid sequence as set forth in any of the sequences shown in SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:46, SEQ ID NO:50, SEQ ID NO:54, SEQ ID NO:58, and SEQ ID NO:60.

Each such protein will preferably include at least 50, or from about 50 to about 100, or from about 50 to about 300 contiguous amino acids present in any full length protein sequence set forth in the sequences referenced above, and the toxin proteins are preferably encoded by a polynucleotide segment that hybridizes under stringent conditions to the polynucleotide coding sequences as set forth in any of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, and SEQ ID NO:63.

Compositions containing the proteins of the present invention are provided in an agriculturally-acceptable carrier. The composition may contain a recombinant *Bacillus thuringiensis* cell extract, cell suspension, cell homogenate, cell lysate, cell supernatant, cell filtrate, or cell pellet in which at least a pest inhibitory amount of one or more of the proteins of the present invention are provided, and the composition can be provided in the form of a powder, dust, pellet, granule, spray, emulsion, colloid, or solution. The composition may be prepared by desiccation, lyophilization, homogenization, extraction, filtration, centrifugation, sedimentation, or concentration of a culture of recombinant *Bacillus thuringiensis* cells or spore crystals containing one or more of the proteins of the present invention. The pesticidal composition preferably contains from about 1% to about 99% by weight of one or more of the pesticidal proteins described herein.

The proteins of the present invention can be obtained in substantially concentrated and/or purified form by a process which may include the steps of i) culturing recombinant *Bacillus thuringiensis* cells containing one or more recombinant polynucleotide as set forth above under conditions effective to produce the pesticidal protein, and obtaining the pesticidal polypeptide so produced. The polypeptide will preferably contain the contiguous amino acid sequence as set forth in any of SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:46, SEQ ID NO:50, SEQ ID NO:54, SEQ ID NO:58, and SEQ ID NO:60.

BRIEF DESCRIPTION OF THE SEQUENCES

SEQ ID NO 1 represents a native Bt nucleotide sequence encoding a ET34 protein.

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SEQ ID NO 2 represents an amino acid sequence translation of SEQ ID NO 1.

SEQ ID NO 3 represents an artificial sequence encoding a ET34 protein.

SEQ ID NO 4 represents an amino acid sequence translation of SEQ ID NO 3 from nucleotide position 1 through nucleotide position 378.

SEQ ID NO 5 represents a nucleotide sequence encoding a P139 secretion signal peptide (nucleotide position 1-75) fused in frame to a native Bt nucleotide sequence encoding a ET34 protein (nucleotide position 76-450).

SEQ ID NO 6 represents the amino acid sequence translation of SEQ ID NO 5.

SEQ ID NO 7 represents a nucleotide sequence encoding a P139 secretion signal peptide (nucleotide position 1-75) fused in frame to a synthetic nucleotide sequence encoding a ET34 protein (nucleotide position 76-450).

SEQ ID NO 8 represents the amino acid sequence translation of SEQ ID NO 7.

SEQ ID NO 9 represents the native Bt nucleotide sequence encoding a TIC1506 protein.

SEQ ID NO 10 represents the amino acid sequence translation of SEQ ID NO 9.

SEQ ID NO 11 represents an artificial nucleotide sequence encoding a TIC1506 protein.

SEQ ID NO 12 represents the amino acid sequence translation of SEQ ID NO 11.

SEQ ID NO 13 represents the native Bt nucleotide sequence encoding a TIC1501 protein.

SEQ ID NO 14 represents the amino acid sequence translation of SEQ ID NO 13.

SEQ ID NO 15 represents an artificial nucleotide sequence encoding a TIC1501 protein.

SEQ ID NO 16 represents the amino acid sequence translation of SEQ ID NO 15.

SEQ ID NO 17 represents the native Bt nucleotide sequence encoding a TIC1503 protein.

SEQ ID NO 18 represents the amino acid sequence translation of SEQ ID NO 17.

SEQ ID NO 19 represents an artificial nucleotide sequence encoding a TIC1503 protein.

SEQ ID NO 20 represents the amino acid sequence translation of SEQ ID NO 19.

SEQ ID NO 21 represents a native Bt nucleotide sequence encoding a TIC614 protein.

SEQ ID NO 22 represents an amino acid sequence translation of SEQ ID NO 21.

SEQ ID NO 23 represents an artificial nucleotide sequence encoding a TIC614 protein.

SEQ ID NO 24 represents an amino acid sequence translation of SEQ ID NO 23.

SEQ ID NO 25 represents a nucleotide sequence encoding a TIC615 protein.

SEQ ID NO 26 represents the amino acid sequence translation of SEQ ID NO 25.

SEQ ID NO 27 represents an artificial nucleotide sequence encoding a TIC615 protein.

SEQ ID NO 28 represents the amino acid sequence translation of SEQ ID NO 27.

SEQ ID NO 29 represents the native Bt nucleotide sequence encoding a TIC1277 protein.

SEQ ID NO 30 represents the amino acid sequence translation of SEQ ID NO 29.

SEQ ID NO 31 represents an artificial nucleotide sequence encoding a TIC1277 protein.

SEQ ID NO 32 represents the amino acid sequence translation of SEQ ID NO 31.

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SEQ ID NO 33 represents the native Bt nucleotide sequence encoding a TIC TIC1278 protein.

SEQ ID NO 34 represents the amino acid sequence translation of SEQ ID NO 33.

SEQ ID NO 35 represents an artificial nucleotide sequence encoding a TIC TIC1278 protein.

SEQ ID NO 36 represents the amino acid sequence translation of SEQ ID NO 35.

SEQ ID NO 37 represents the native Bt nucleotide sequence encoding a TIC TIC1310 protein.

SEQ ID NO 38 represents the amino acid sequence translation of SEQ ID NO 37.

SEQ ID NO 39 represents an artificial nucleotide sequence encoding a TIC1310 protein.

SEQ ID NO 40 represents the amino acid sequence translation of SEQ ID NO 39.

SEQ ID NO 41 represents the native Bt nucleotide sequence encoding a TIC TIC1311 protein.

SEQ ID NO 42 represents the amino acid sequence translation of SEQ ID NO 41.

SEQ ID NO 43 represents an artificial nucleotide sequence encoding a TIC1311 protein.

SEQ ID NO 44 represents the amino acid sequence translation of SEQ ID NO 43.

SEQ ID NO 45 represents the native Bt nucleotide sequence encoding a TIC1324 protein.

SEQ ID NO 46 represents the amino acid sequence translation of SEQ ID NO 45.

SEQ ID NO 47 represents an artificial nucleotide sequence encoding a TIC1324 protein.

SEQ ID NO 48 represents the amino acid sequence translation of SEQ ID NO 47.

SEQ ID NO 49 represents the native Bt nucleotide sequence encoding a TIC1407 protein.

SEQ ID NO 50 represents the amino acid sequence translation of SEQ ID NO 49.

SEQ ID NO 51 represents an artificial nucleotide sequence encoding a TIC TIC1407 protein.

SEQ ID NO 52 represents the amino acid sequence translation of SEQ ID NO 51.

SEQ ID NO 53 represents the native Bt nucleotide sequence encoding a TIC TIC1408 protein.

SEQ ID NO 54 represents the amino acid sequence translation of SEQ ID NO 53.

SEQ ID NO 55 represents an artificial nucleotide sequence encoding a TIC1408 protein.

SEQ ID NO 56 represents the amino acid sequence translation of SEQ ID NO 56.

SEQ ID NO 57 represents a native Bt nucleotide sequence encoding a TIC1308 protein.

SEQ ID NO 58 represents an amino acid sequence translation of SEQ ID NO 57.

SEQ ID NO 59 represents a native Bt nucleotide sequence encoding a TIC1442 protein.

SEQ ID NO 60 represents an amino acid sequence translation of SEQ ID NO 59.

SEQ ID NO 61 represents an artificial nucleotide sequence encoding a TIC1308 protein.

SEQ ID NO 62 represents an amino acid sequence translation of SEQ ID NO 61.

SEQ ID NO 63 represents an artificial nucleotide sequence encoding a TIC1442 protein.

SEQ ID NO 64 represents an amino acid sequence translation of SEQ ID NO 63.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to methods and compositions for pest control in plants, in particular nematode and/or insect control.

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In one aspect, the invention relates to controlling, preventing or treating nematode and/or insect infection in transgenic plants. The method comprises, in one embodiment, generation of transgenic plants containing a recombinant construct and expression of such construct to impart such pest resistance to plants. The recombinant construct may comprise a nucleotide sequence encoding one or more proteins, wherein the sequence is operably linked to a heterologous promoter functional in a plant cell, and to cells transformed with the recombinant construct. Cells comprising (meaning including but not limited to) the recombinant construct may be prokaryotic or eukaryotic. In particular, eukaryotic cells may be plant cells. Plants and seeds derived from such transformed plant cells are also contemplated. The transgenic plants or parts thereof of the present invention, in one embodiment, produce one or more pesticidal proteins derived from *Bacillus thuringiensis* bacterial strains.

The present invention provides heterologous molecules that are expressed in the cytoplasm of the host cell, or if used in a eukaryotic cell such as a plant cell, may also be directed into the plastid of the plant to provide production of the toxic protein, and including, but not limited to, nucleotide segments that encode polypeptides such as SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:46, SEQ ID NO:50, SEQ ID NO:54, SEQ ID NO:58, and SEQ ID NO:60 having pesticidal activity. In certain embodiments, the polypeptide having pesticidal activity may share at least about 45%, or at least about 50%, or at least about 51-79%, or at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 98%, or at least 99%, or 100% sequence identity, to any one or more amino acid sequence(s) set forth in SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:46, SEQ ID NO:50, SEQ ID NO:54, SEQ ID NO:58, or SEQ ID NO:60. The function of the encoded polypeptide may also be determined by measuring the efficacy of the presence of the transgene that encodes it in reducing nematode and/or insect infection, growth, reproduction, or symptomology. For instance, a reduction in root galls, cysts, or worm number of 20% or more, 25% or more, 50% or more, 80% or more, or 95% or more, in a transgenic plant comprising a heterologous nucleotide construct encoding any of the proteins of the present invention, relative to a control plant, for instance an otherwise isogenic plant not comprising the heterologous molecule, under similar conditions, indicates the presence of a functional molecule.

In certain embodiments, a heterologous molecule provided by the present invention that is directed into the plastid of a plant to provide production of a toxin protein of the present invention may share at least from about 60 to about 79%, or at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 98%, or at least 99%, or 100% sequence identity at the nucleotide level with one or more sequence(s) as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, and SEQ ID NO:63.

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Thus, in particular embodiments, the heterologous molecule may comprise a sequence encoding a heterologous chloroplast transit peptide.

Yet another aspect of the invention provides methods for production and for use of one or more of the proteins of the present invention to control nematode and/or insect infestation. Thus, methods for production of a toxin, for instance in a plant cell, are provided. The toxin may then be applied to soil prior to, during, or subsequent to planting of a crop, in order to control or reduce nematode infestation or symptomatology of crop plants grown in that soil.

Unless otherwise noted, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art. Definitions of common terms in molecular biology may also be found in Rieger et al., *Glossary of Genetics: Classical and Molecular*, 5th edition, Springer-Verlag: New York, 1991; and Lewin, *Genes V*, Oxford University Press: New York, 1994. The nomenclature for DNA bases as set forth at Title 37 of the United States Code of Federal Regulations, Part 1, section 1.822.

As used herein, a “transgenic plant” is any plant in which one or more, or all, of the cells of the plant include a transgene. A transgene may be integrated within a nuclear genome or organelle genome, or it may be extra-chromosomally replicating DNA. The term “transgene” means a nucleic acid that is partly or entirely heterologous, foreign, to a transgenic microbe, plant, animal, or cell into which it is introduced. Cells that make up various cell and tissue types of plants include but are not limited to seed, root, leaf, shoot, flower, pollen and ovule.

“Recombinant DNA” is a polynucleotide having a genetically engineered modification introduced through combination of endogenous and/or exogenous molecules in a transcription unit, manipulation via mutagenesis, restriction enzymes, and the like or simply by inserting multiple copies of a native transcription unit. Recombinant DNA may comprise DNA segments obtained from different sources, or DNA segments obtained from the same source, but which have been manipulated to join DNA segments which do not naturally exist in the joined form. An isolated recombinant polynucleotide may exist, for example as a purified molecule, or integrated into a genome, such as a plant cell, or organelle genome or a microbe plasmid or genome. The polynucleotide comprises linked regulatory molecules that cause transcription of an RNA in a plant cell.

As used herein, “percent identity” means the extent to which two optimally aligned DNA or protein segments are invariant throughout a window of alignment of components, for example nucleotide sequence or amino acid sequence. An “identity fraction” for aligned segments of a test sequence and a reference sequence is the number of identical components that are shared by sequences of the two aligned segments divided by the total number of sequence components in the reference segment over a window of alignment which is the smaller of the full test sequence or the full reference sequence. “Percent identity” (“% identity”) is the identity fraction times 100.

“Expression” means transcription of DNA to produce RNA. The resulting RNA may be without limitation mRNA encoding a protein, antisense RNA, or a double-stranded RNA for use in RNAi technology. Expression also may refer to translation of RNA, i.e. the production of encoded protein from an mRNA.

As used herein, “promoter” means regulatory DNA molecules for initializing transcription. A “plant promoter” is a promoter capable of initiating transcription in plant cells whether or not its origin is a plant cell. For example it is well

known that certain *Agrobacterium* promoters are functional in plant cells. Thus, plant promoters include promoter DNA obtained from plants, plant viruses (in particular, double stranded DNA viruses) and bacteria such as *Agrobacterium* and *Bradyrhizobium* bacteria. Constitutive promoters generally provide transcription in most or all of the cells of a plant. In particular, promoters such as the FMV promoter (FMV, U.S. Pat. No. 6,051,753), the enhanced 35S promoter (E35S, U.S. Pat. No. 5,359,142), rice actin promoter (U.S. Pat. No. 5,641,876), and various chimeric promoters (U.S. Pat. No. 6,660,911) are useful in the present invention. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, or seeds. Such promoters are referred to as "tissue-preferred". Promoters that initiate transcription only in certain tissues are referred to as "tissue specific."

A number of root-specific or root-enhanced promoters or fragments of such that provide enhanced expression in root tissues relative to other plant tissues have been identified and are known in the art (e.g. U.S. Pat. Nos. 5,110,732, 5,837,848, 5,837,876; 5,633,363; 5,459,252; 5,401,836; 7,196,247; 7,232,940; 7,119,254; and 7,078,589). Examples include root-enhanced or root-specific promoters such as the CaMV-derived as-1 promoter or the wheat POX1 promoter (U.S. Pat. No. 5,023,179), the acid chitinase gene promoter (Samac et al., *Plant Mol. Biol.* 25:587-596 (1994); the root specific subdomains of the CaMV35S promoter (Lam et al., *Proc. Natl. Acad. Sci. (U.S.A.)* 86:7890-7894 (1989); the root-enhanced ORF13 promoter from *Agrobacterium rhizogenes* (Hansen et al., *Mol. Gen. Genet.* 254:337-343 (1997); the promoter for the tobacco root-specific gene RB7 (U.S. Pat. No. 5,750,386); and the root cell-specific promoters reported by Conkling et al. (*Plant Physiol.* 93:1203-1211 (1990). Additional examples include RCC2 and RCC3, promoters that direct root-specific gene transcription in rice (Xu et al., *Plant Mol. Biol.* 27:237, 1995); soybean root-specific glutamine synthetase promoter (Hire et al., *Plant Mol. Biol.* 20:207-218, 1992); root-specific control element in the GRP 1.8 gene of French bean (Keller and Baumgartner, *Plant Cell* 3:1051-1061, 1991.); a root-specific promoter of the mannopine synthase (MAS) gene of *Agrobacterium tumefaciens* (Sanger et al., *Plant Mol. Biol.* 14:433-443, 1990); and full-length cDNA clone encoding cytosolic glutamine synthetase (GS), which is expressed in roots and root nodules of soybean (Miao et al., *Plant Cell* 3:11-22, 1991). See also Bogusz et al., *Plant Cell* 2:633-641, 1990, where two root-specific promoters isolated from hemoglobin genes from the nitrogen-fixing non-legume *Parasponia andersonii* and the related non-nitrogen-fixing non-legume *Trema tomentosa* are described. Leach and Aoyagi (1991) describe their analysis of the promoters of the highly expressed rolC and rolD root-inducing genes of *Agrobacterium rhizogenes* (see *Plant Science* (Limerick) 79:69-76). Additional root-preferred promoters include the VFENOD-GRP3 gene promoter (Kuster et al., *Plant Mol. Biol.* 29(4):759-772, 1995); and rolB promoter (Capana et al., *Plant Mol. Biol.* 25:681-691, 1994). Examples of nematode-induced promoters include, for instance, the TobRB7 promoter (Opperman et al., *Science* 263:221-223, 1994), and promoters described in U.S. Pat. Nos. 6,262,344, and 7,193,136.

The term "resistance," or "tolerance" when used in the context of comparing the effectiveness of a transgene in a transgenic plant, refers to the ability of the transgenic plant to maintain a desirable phenotype when exposed to nematode infestation pressures relative to the phenotype presented by a nematode sensitive non-transgenic plant under similar conditions. The level of resistance can be determined by compar-

ing the physical characteristics of the transgenic plant to non-transgenic plants that either have or have not been exposed to nematode and/or insect infection. Exemplary physical characteristics to observe include plant height, an increase in population of plants that have ability to survive nematode or insect challenge (that is, plants that come in contact with a parasitic nematode or insect may have enhanced root growth, enhanced fruit or grain yield, and decreased reproduction of the nematode or insect infesting the plant or crop, or a decrease in the rate of increase if the pest population). The product of expression of the recombinant DNA may be directly toxic to the nematode (nematicidal) or insect (insecticidal), or may affect the mobility, host finding, feeding site establishment, fecundity or have other nematostatic and/or insectic inhibitory effects.

"Transformed seed" is the seed which has been generated from the transformed plant. A transformed plant contains transformed cells. A transformed cell is a cell that has been altered by the introduction of an exogenous DNA molecule or in the present invention comprises a heterologous DNA encoding one or more of the proteins of the present invention.

Pests intended to be within the scope of the present invention include the "lepidopteran pest population" such as *Spodoptera frugiperda*, *Spodoptera exigua*, *Mamestra configurata*, *Agrotis ipsilon*, *Trichoplusia ni*, *Pseudoplusia includens*, *Anticarsia gemmatalis*, *Hypena scabra*, *Heliothis virescens*, *Agrotis subterranea*, *Pseudaletia unipuncta*, *Agrotis orthogonia*, *Ostrinia nubilalis*, *Amyelois transitella*, *Crambus caliginosellus*, *Herpetogramma licarsialis*, *Homoeosoma electellum*, *Elasmopalpus lignosellus*, *Cydia pomonella*, *Endopiza viteana*, *Grapholita molesta*, *Suleima helianthana*, *Plutella xylostella*, *Pectinophora gossypiella*, *Lymantria dispar*, *Blatta orientalis*, *Blatella asahinai*, *Blattella germanica*, *Supella longipalpa*, *Periplaneta americana*, *Periplaneta brunnea*, *Leucophaea maderae*, *Alabama argillacea*, *Archips argyrospila*, *A. rosana*, *Chilo suppressalis*, *Cnaphalocrocis medinalis*, *Crambus caliginosellus*, *C. teterrellus*, *Diatraea grandiosella*, *D. saccharalis*, *Earias insulana*, *E. vittella*, *Helicoverpa armigera*, *H. zea*, *Heliothis virescens*, *Herpetogramma licarsialis*, *Lobesia botrana*, *Pectinophora gossypiella*, *Phyllocoptis citrella*, *Pieris brassicae*, *P. rapae*, *Plutella xylostella*, *Spodoptera exigua*, *S. litura*, *S. frugiperda*, and *Tuta absoluta*. The "coleopteran pest population" includes *Anthonomus grandis*, *Lissorhoptrus oryzophilus*, *Sitophilus granaries*, *Sitophilus oryzae*, *Hypera punctata*, *Sphenophorus maidis*, *Leptinotarsa decemlineata*, *Diabrotica virgifera virgifera*, *Diabrotica barberi*, *Diabrotica undecimpunctata howardi*, *Chaetocnema pulicaria*, *Phyllotreta cruciferae*, *Colaspis brunnea*, *Oulema melanopus*, *Zygogramma exclamationis*, *Epilachna varivestis*, *Popillia japonica*, *Cyclocephala borealis*, *Cyclocephala immaculata*, *Rhizotrogus majalis*, *Phyllophaga crinita*, *Ligyrus gibbosus*, *Melanotus spp.*, *Conoderus spp.*, *Limonius spp.*, *Agriotes spp.*, *Ctenicera spp.*, and *Aeolus spp.*, *Eleodes spp.* The "plant pathogenic nematode population" includes plant parasitic species, for example, *Heterodera* species, *Globodera* species, *Meloidogyne* species, *Rotylenchulus* species, *Hoplolaimus* species, *Belonolaimus* species, *Pratylenchus* species, *Longidorus* species, *Paratrichodorus* species, *Ditylenchus* species, *Xiphinema* species, *Dolichodorus* species, *Helicotylenchus* species, *Radopholus* species, *Hirschmanniella* species, *Tylenchorhynchus* species, and *Trichodorus* species, and the like, and specifically includes *Heterodera glycines* (soybean cyst nematode), *Heterodera schachtii* (beet cyst nematode), *Heterodera avenae*, *Globodera rostochiensis*, *Globodera pailida*, *Pratylenchus zeae* (a root knot nema-

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tode), *Meloidogyne javanica*, *Pratylenchus brachyurus* (a root knot nematode), *Meloidogyne hapla*, and *Meloidogyne incognita*.

The present invention provides recombinant DNA constructs comprising a polynucleotide that, when incorporated in a plant cell, imparts to the plant resistance to nematode and/or insect infection or plant disease caused by such infection (also referred to as infestation). Such constructs also typically comprise a promoter operatively linked to said polynucleotide to provide for expression in the plant cells. Other construct components may include additional regulatory molecules, such as 5' leader regions or 3' untranslated regions (such as polyadenylation sites), intron regions, and transit or signal peptides. Such recombinant DNA constructs can be assembled using methods known to those of ordinary skill in the art.

Recombinant constructs prepared in accordance with the present invention also generally include a 3' untranslated DNA region (UTR) that typically contains a polyadenylation sequence following the polynucleotide coding region. Examples of useful 3' UTRs include but are not limited to those from the nopaline synthase gene of *Agrobacterium tumefaciens* (nos), a gene encoding the small subunit of a ribulose-1,5-bisphosphate carboxylase-oxygenase (rbcS), and the T7 transcript of *Agrobacterium tumefaciens*.

Constructs and vectors may also include a transit peptide for targeting of a protein product, particularly to a chloroplast, leucoplast or other plastid organelle, mitochondria, peroxisome, or vacuole or an extracellular location. For descriptions of the use of chloroplast transit peptides, see U.S. Pat. No. 5,188,642 and U.S. Pat. No. 5,728,925. Many chloroplast-localized proteins are expressed from nuclear genes as precursors and are targeted to the chloroplast by a chloroplast transit peptide (CTP). Examples of other such isolated chloroplast proteins include, but are not limited to those associated with the small subunit (SSU) of ribulose-1,5,-bisphosphate carboxylase, ferredoxin, ferredoxin oxidoreductase, the light-harvesting complex protein I and protein II, thioredoxin F, enolpyruvyl shikimate phosphate synthase (EPSPS) and transit peptides described in U.S. Pat. No. 7,193,133. It has been demonstrated in vivo and in vitro that non-chloroplast proteins may be targeted to the chloroplast by use of protein fusions with a heterologous CTP and that the CTP is sufficient to target a protein to the chloroplast. Incorporation of a suitable chloroplast transit peptide, such as, the *Arabidopsis thaliana* EPSPS CTP (CTP2, Klee et al., *Mol. Gen. Genet.* 210:437-442, 1987), and the *Petunia hybrida* EPSPS CTP (CTP4, della-Cioppa et al., *Proc. Natl. Acad. Sci. USA* 83:6873-6877, 1986) has been shown to target heterologous EPSPS protein sequences to chloroplasts in transgenic plants. The production of glyphosate tolerant plants by expression of a fusion protein comprising an amino-terminal CTP with a glyphosate resistant EPSPS enzyme is well known by those skilled in the art, (U.S. Pat. No. 5,627,061, U.S. Pat. No. 5,633,435, U.S. Pat. No. 5,312,910, EP 0218571, EP 189707, EP 508909, and EP 924299). Those skilled in the art will recognize that various chimeric constructs can be made that utilize the functionality of a CTP to import various pesticidal proteins of the present invention into the plant cell plastid.

Stable methods for plant transformation include virtually any method by which DNA can be introduced into a cell, such as by direct delivery of DNA (for example, by PEG-mediated transformation of protoplasts, by electroporation, by agitation with silicon carbide fibers, and by acceleration of DNA coated particles), by *Agrobacterium*-mediated transformation, by viral or other vectors. One preferred method of plant transformation is microprojectile bombardment, for

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example, as illustrated in U.S. Pat. No. 5,015,580 (soy), U.S. Pat. No. 5,550,318 (maize), U.S. Pat. No. 5,538,880 (maize), U.S. Pat. No. 6,153,812 (wheat), U.S. Pat. No. 6,160,208 (maize), U.S. Pat. No. 6,288,312 (rice) and U.S. Pat. No. 6,399,861 (maize), and U.S. Pat. No. 6,403,865 (maize).

Detailed procedures for *Agrobacterium*-mediated transformation of plants, especially crop plants, include, for example, procedures disclosed in U.S. Pat. Nos. 5,004,863, 5,159,135, 5,518,908, 5,846,797, and 6,624,344 (cotton); U.S. Pat. Nos. 5,416,011, 5,569,834, 5,824,877, 5,914,451 6,384,301, and 7,002,058 (soy); U.S. Pat. Nos. 5,591,616 5,981,840, and 7,060,876 (maize); U.S. Pat. Nos. 5,463,174 and 5,750,871 (*Brassica* species, including rapeseed and canola), and in U.S. Patent Application Publications 2004/0244075 (maize), 2004/0087030 (cotton) and 2005/0005321 (soybean). Additional procedures for *Agrobacterium*-mediated transformation are disclosed in WO9506722 (maize). Similar methods have been reported for many plant species, both dicots and monocots, including, among others, peanut (Cheng et al., *Plant Cell Rep.*, 15:653, 1996); asparagus (Bytebier et al., *Proc. Natl. Acad. Sci. U.S.A.*, 84:5345, 1987); barley (Wan and Lemaux, *Plant Physiol.*, 104:37, 1994); rice (Toriyama et al., *Bio/Technology*, 6:10, 1988; Zhang et al., *Plant Cell Rep.*, 7:379, 1988; wheat (Vasil et al., *Bio/Technology*, 10:667, 1992; Becker et al., *Plant J.*, 5:299, 1994), alfalfa (Masoud et al., *Transgen. Res.*, 5:313, 1996); *Brassica* species (Radke et al., *Plant Cell Rep.*, 11:499-505, 1992); and tomato (Sun et al., *Plant Cell Physiol.*, 47:426-431, 2006). Transgenic plant cells and transgenic plants can also be obtained by transformation with other vectors, such as but not limited to viral vectors (for example, tobacco etch virus (TEV), barley stripe mosaic virus (BSMV), and the viruses referenced in Edwards and Christie, "The Potyvirus Group Monograph No. 16", 1991, Agric. Exp. Station, Univ. of Florida), plasmids, cosmids, YACs (yeast artificial chromosomes), BACs (bacterial artificial chromosomes) or any other suitable cloning vector, when used with an appropriate transformation protocol such as but not limited to bacterial infection (for example, with *Agrobacterium* as described above), binary bacterial artificial chromosome constructs, direct delivery of DNA (for example, via PEG-mediated transformation, desiccation/inhibition-mediated DNA uptake, electroporation, agitation with silicon carbide fibers, and microprojectile bombardment). It would be clear to one of ordinary skill in the art that various transformation methodologies can be used and modified for production of stable transgenic plants from any number of plant species of interest. For example the construction of stably inherited recombinant DNA constructs and mini-chromosomes can be used as vectors for the construction of transgenic plants (U.S. Pat. No. 7,235,716).

Plants of the present invention include, but are not limited to, *Acacia*, alfalfa, aneth, apple, apricot, artichoke, arugula, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussels sprouts, cabbage, canola, cantaloupe, carrot, cassava, cauliflower, celery, cherry, cilantro, citrus, clementine, coffee, corn, cotton, cucumber, Douglas fir, eggplant, endive, escarole, eucalyptus, fennel, figs, forest trees, gourd, grape, grapefruit, honey dew, jicama, kiwifruit, lettuce, leeks, lemon, lime, loblolly pine, mango, melon, mushroom, nut, oat, okra, onion, orange, an ornamental plant, papaya, parsley, pea, peach, peanut, pear, pepper, persimmon, pine, pineapple, plantain, plum, pomegranate, poplar, potato, pumpkin, quince, radiata pine, radicchio, radish, rapeseed, raspberry, rice, rye, sorghum, Southern pine, soybean, spinach, squash, strawberry, sugarbeet, sugarcane, sunflower, sweet potato, sweetgum, tangerine, tea, tobacco, tomato, turf, a vine, watermelon, wheat, yams, and zucchini. Crop plants

are defined as plants which are cultivated to produce one or more commercial products. Examples of such crops or crop plants include but are not limited to soybean, canola, rape, cotton (cottonseeds), peanut, sunflower, pigeon pea, chick-pea, and the like, and grains such as corn, wheat, rice, oat, millet, and rye, and the like. Rape, rapeseed and canola are used synonymously in the present disclosure.

Transformation methods to provide transgenic plant cells and transgenic plants containing stably integrated recombinant DNA are preferably practiced in tissue culture on media and in a controlled environment. Recipient cell targets include but are not limited to meristem cells, callus, immature embryos or parts of embryos, gametic cells such as microspores, pollen, sperm, and egg cells. Any cell from which a fertile plant can be regenerated is contemplated as a useful recipient cell for practice of the invention. Callus can be initiated from various tissue sources, including, but not limited to, immature embryos or parts of embryos, seedling apical meristems, microspores, and the like. Those cells which are capable of proliferating as callus can serve as recipient cells for genetic transformation. Practical transformation methods and materials for making transgenic plants of this invention (for example, various media and recipient target cells, transformation of immature embryos, and subsequent regeneration of fertile transgenic plants) are disclosed, for example, in U.S. Pat. Nos. 6,194,636 and 6,232,526 and U.S. Patent Application Publication 2004/0216189.

In general transformation practice, DNA is introduced into only a small percentage of target cells in any one transformation experiment. Marker genes are generally used to provide an efficient system for identification of those cells that are transformed by a transgenic DNA construct. Preferred marker genes provide selective markers which confer resistance to a selective agent, such as an antibiotic or herbicide. Any of the antibiotics or herbicides to which a plant cell may be resistant can be a useful agent for selection. Potentially transformed cells are exposed to the selective agent. In the population of surviving cells will be those cells where, generally, the resistance-conferring gene is expressed at sufficient levels to permit cell survival in the presence of the selective agent. Cells can be tested further to confirm integration of the recombinant DNA. Commonly used selective marker genes include those conferring resistance to antibiotics such as kanamycin or paromomycin (val), hygromycin B (aph IV), gentamycin (aac3 and aacC4) and glufosinate (bar or pat), glyphosate (EPSPS), and dicamba (dicamba monooxygenase). Examples of useful selective marker genes and selection agents are illustrated in U.S. Pat. Nos. 5,550,318, 5,633,435, 5,780,708, and 6,118,047. Screenable markers or reporters, such as markers that provide an ability to visually identify transformants can also be employed. Non-limiting examples of useful screenable markers include, for example, a gene expressing a protein that produces a detectable color by acting on a chromogenic substrate (for example, beta-glucuronidase, GUS, uidA, or luciferase, luc) or that itself is detectable, such as green fluorescent protein (GFP, gfp) or an immunogenic molecule. Those of skill in the art will recognize that many other useful markers or reporters are available for use.

The recombinant DNA constructs of the invention can be stacked with other recombinant DNA for imparting additional agronomic traits (such as in the case of transformed plants, traits including but not limited to herbicide resistance, insect resistance, cold germination tolerance, water deficit tolerance, enhanced yield, enhanced quality, fungal, viral, and bacterial disease resistance) for example, by expressing other transgenes. The recombinant DNA constructs of the

present invention can also be transformed into plant varieties that carry natural pest or pathogen resistance genes to enhance the efficacy of the resistance phenotype. Constructs for coordinated decrease and/or increase of gene expression are disclosed in U.S. Patent Application Publication 2004/0126845 A1. Seeds of transgenic, fertile plants can be harvested and used to grow progeny generations, including hybrid generations, of transgenic plants of this invention that include the recombinant DNA construct in their genome. Thus, in addition to direct transformation of a plant with a recombinant DNA construct of this invention, transgenic plants of the invention can be prepared by crossing a first plant having the recombinant DNA with a second plant lacking the construct. For example, the recombinant DNA can be introduced into a plant line that is amenable to transformation to produce a transgenic plant, which can be crossed with a second plant line to introgress the recombinant DNA into the resulting progeny. A transgenic plant of the invention can be crossed with a plant line having other recombinant DNA or naturally occurring genetic regions that confers one or more additional trait(s) (such as, but not limited to, herbicide resistance, pest or disease resistance, environmental stress resistance, modified nutrient content, and yield improvement) to produce progeny plants having recombinant DNA that confers both the desired target sequence expression behavior and the additional trait(s). Typically, in such breeding for combining traits the transgenic plant donating the additional trait is a male line and the transgenic plant carrying the base traits is the female line. The progeny of this cross segregate such that some of the plant will carry the DNA for both parental traits and some will carry DNA for one parental trait; such plants can be identified by markers associated with parental recombinant DNA. Progeny plants carrying DNA for both parental traits can be crossed back into the female parent line multiple times, for example, usually 6 to 8 generations, to produce a progeny plant with substantially the same genotype as one original transgenic parental line but for the recombinant DNA of the other transgenic parental line.

Other proteins and toxic agents can be used together with one or more proteins of the present invention to control plant pathogenic nematode and/or insect infestation and to reduce the likelihood of development of resistance to any single method of control. Such other proteins and toxic agents include but are not limited to, as applicable to either nematode or insect control, methylketone synthase, dsRNA expressed in the cell and targeting for suppression one or more essential, housekeeping, reproductive or developmental gene, other proteins that are known in the art to be toxic to plant pathogenic nematodes or insects such as Cry and VIP proteins (lifesci.sussex.ac.uk/home/Neil_Crickmore/Bt/index.html) on the world wide web, which is properly referenced as Crickmore et. al. (2010) "Bacillus thuringiensis toxin nomenclature", as well as chemical nematicides used in seed treatments or soil drenches. Topically applied dsRNA methods are also known in the art that can be applied to a plant expressing one or more of the proteins of the present invention. Such topical applications can be effective in causing a systemic effect in the plant that result in nematode or insect control by applying to the plant a dsRNA molecule that targets for regulation a gene in the plant involved in such resistance. All such combinations are within the scope of the present invention.

The transgenic plant, plant part, seed or progeny plants of the present invention can be processed into products useful in commerce. These products, commodity products, include but are not limited to meal, flour, oil, hay, starch, juice, protein extract, and fiber.

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The proteins of the present invention have been identified using a variety of methods. One method has been to identify previously known Bt proteins that exhibit a mass less than about 40 kDa, or less than about 35 kDa, or less than about 30 kDa, or less than about 28 kDa, or less than about 25 kDa, or less than about 20 kDa, or less than about 15 kDa. Such proteins include but are not limited to the smaller component of most known binary Bt toxins, such as Cry34/35 (PS149B1), TIC100/101, ET33/34, ET80/76, and the like. Other proteins known in the art include TIC901, TIC1201, TIC407, TIC417, TIC431, ET70, VIP proteins such as VIP3Aa and the like, which are all generally small toxin proteins that are known to exhibit insecticidal activity. The inventors herein have identified that such smaller toxin molecules, when provided in the diet of a *C. elegans* nematode, exhibit various levels of inhibitory effects. Surprisingly, it has also been observed that the nematicidal activity of these proteins can be imparted through the diet of a cyst nematode more effectively by truncating the proteins to smaller sizes, whether truncated at the C terminus, the N terminus, or both. Truncated versions typically exhibit a mass of from about 14 to about 28-30 kDa, and exhibit improved bioactivity likely because the ability of the cyst nematode to uptake proteins larger than about 30 kDa is limited (Urwin et al. ((1997) Plant J. 12:455) and Bockenhoff & Grundler ((1994) Parasitology 109:249). TIC1501 (about 27 kDa), TIC1503 (about 34 kDa), and TIC1506 (about 36 kDa) represent various fragments of the TIC1201 protein, 1201 being previously shown to exhibit coleopteran toxic effects. Surprisingly, the truncated versions less than 36 kDa exhibit significant nematicidal effects.

Proteins of the present invention have also been identified de novo, and these include the proteins listed herein as TIC614, TIC615, TIC1277, TIC1278, TIC1308, TIC1310, TIC1311, TIC1324, TIC1407, TIC1408, and TIC1442. Such proteins were identified by various methods, whether being directly amplified from various Bt strain genomes, or identified by high throughput sequence analysis of various Bt genomes. In either case, genomic DNA segments are obtained and analyzed using bioinformatic techniques that result in the identification of all or portions of open reading frames encoding protein segments. The resulting protein segments are then characterized versus all known protein sequences in the art, and to the extent that there is any similarity to a toxin molecule, the complete sequence of the open reading frame encoding the protein is obtained. Proteins that are identified that exhibit a mass of less than about 40 kDa, or preferably less than about 30 kDa are then evaluated in a *C. elegans* assay to determine if any effects are observed relative to *C. elegans* survival. Toxins exhibiting nematicidal properties are then evaluated for other pesticidal properties, particularly insecticidal activity. Surprisingly, the above referenced proteins all exhibited nematicidal activity, and some exhibited insecticidal activity as reported in the examples below.

EXAMPLES

The following examples are illustrative of the invention, which may be embodied in various forms and are not to be interpreted as limiting the scope or content of the disclosure in any way.

Example 1

DNA Molecules Encoding Bt Toxin Proteins

Toxin ET34 (SEQ ID NO:1) has been previously described (U.S. Pat. No. 6,063,756). A secretion signal from the gene

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P139 (First 75 nucleotide of SEQ ID NO:1 from the WIPO Publication Number WO9408010) was operably linked to the 5' end of the ET34 (SEQ ID NO:5) to enable its secretion outside the plasma membrane to avoid potential toxicity to the plant cell and to allow easy access of the protein to the pest.

TIC1506 (SEQ ID NO:9), TIC1501 (SEQ ID NO:13), and TIC 1503 (SEQ ID NO:17) are Bt nucleotide of various fragments of TIC1201 which is 364 amino acids long as set forth in SEQ ID NO 6 of US Patent Application Publication Number US2006-0191034 A1. TIC1506 is 321 amino acids long without the putative N terminal signal peptide of TIC1201 and contains amino acid 44 to 364 of TIC1201 with a methionine residue substituted for the native alanine residue at amino acid position 44. TIC1501 is 227 amino acids long without the putative N terminal signal peptide and a portion of the C terminal of TIC1201 and contains amino acids 44 to 270 of TIC1201 with a methionine residue substituted for the native alanine residue at position 44. TIC1503 is 301 amino acids long without the putative N terminal signal peptide and a portion of the C terminal of TIC1201 and contains amino acids 44 to 344 of TIC1201 with a methionine residue substituted for the native alanine residue at position 44.

Proteins exhibiting pesticidal properties have been identified in various Bt strains. Open reading frames encoding the amino acid sequences, TIC614 (SEQ ID NO: 22), TIC615 (SEQ ID NO: 26), TIC1277 (SEQ ID NO: 30), TIC1278 (SEQ ID NO: 34), TIC1310 (SEQ ID NO: 38), TIC1311 (SEQ ID NO: 42), TIC1324 (SEQ ID NO: 46), TIC1407 (SEQ ID NO: 50), and TIC1408 (SEQ ID NO: 54), exhibiting various degrees of homology to previously known Bt toxin segments were identified. Complete forward and reverse sequence analysis of such open reading frames resulted in the identification of deduced amino acid compositions that exhibit the size and potential for pesticidal (nematicidal and/or insecticidal) activity.

Proteins exhibiting pesticidal properties have been identified in various Bt strains. Open reading frames encoding the amino acid sequences, TIC1308 (SEQ ID NO: 58) and TIC1442 (SEQ ID NO: 60), exhibiting various degrees of homology to previously known Bt toxin segments were identified. Complete forward and reverse sequence analysis of such open reading frames resulted in the identification of deduced amino acid compositions that exhibit the size and potential for pesticidal (nematicidal and/or insecticidal) activity.

Example 2

Expression of Pesticidal Polypeptides from Polynucleotides

Open reading frames of ET34 (SEQ ID NO: 1), P139-ET34 (SEQ ID NO: 5), TIC1506 (SEQ ID NO:9), TIC1501 (SEQ ID NO:13), TIC 1503 (SEQ ID NO:17), TIC614 (SEQ ID NO:21), TIC615 (SEQ ID NO:25), TIC1277 (SEQ ID NO:29), TIC1278 (SEQ ID NO:33), TIC1310 (SEQ ID NO:37), TIC1311 (SEQ ID NO:41), TIC1324 (SEQ ID NO:45), TIC1407 (SEQ ID NO:49), TIC1408 (SEQ ID NO:53), TIC1308 (SEQ ID NO: 57), and TIC1442 (SEQ ID NO: 59) encoding the deduced amino acid compositions exemplified in Example 1 were cloned into a Bt/*E. coli* shuttle plasmid enabling the expression of the deduced amino acid composition in either an acrystalliferous Bt strain or in an *E. coli* bacterium. Recombinant plasmids were transformed into an acrystalliferous Bt expression host after confirming the DNA sequence of the polynucleotide encoding the polypep-

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tide. The gene of interest was cloned downstream of either a *Bacillus* vegetative stage or sporulation stage specific promoter to allow the protein to be expressed respectively during vegetative growth or during sporulation of the recombinant Bt strain. Conditions for vegetative expression of the protein included growing the cells for 24-48 hrs in Terrific Broth medium at 25-28° C. Crystal formation is one characteristic of certain Bt toxin proteins. Proteins that were confirmed to produce crystals when expressed in the acrystalliferous Bt strain were further evaluated. Certain proteins accumulated in the cells and/or were secreted into the culture medium. Both the cell pellets and the culture were analyzed by SDS-PAGE for expression of the expected protein. Conditions for expression from a sporulation specific promoter included growing the cells for 96 hrs at 25-28° C. in C2 medium. Protein crystals were formed during sporulation and released from lysed cells as sporulation was completed. Spores and crystals were collected by centrifugation at 4000×g for 20 minutes, resuspended in wash buffer (10 mM Tris, 0.1 mM EDTA and 0.005% Triton X100 pH 6.8) and collected again by centrifugation. The spore-crystals pellets were then resuspended in $\frac{1}{10}$ th of the original culture volume. The 10x concentrated spore-crystal preparation were analyzed by SDS-PAGE the presence of the expected protein.

Example 3

Nematode and Insect Bioassays

C. elegans feeding screens have been successfully used to identify plant pathogenic nematode-active toxins, for example for SCN and RKN from the order Tylenchida (Wei et al., 2003, PNAS, USA, 100: 2760). The proteins of the present invention were expressed and provided in the diet of a *C. elegans* nematode, essentially following the method of Wei et al. Efficacy was scored on a scale of 1-3, where a score of 1 represents normal health and reproduction of *C. elegans*, and a score of 3 represents no reproduction or poor health of *C. elegans*. Toxins ET34 (SEQ ID NO: 2), TIC1501 (SEQ ID NO: 14), TIC1503 (SEQ ID NO: 18), TIC614 (SEQ ID NO:22), TIC615 (SEQ ID NO:26), TIC1277 (SEQ ID NO:30), TIC1278 (SEQ ID NO:34), TIC1310 (SEQ ID NO:38), TIC1311 (SEQ ID NO:42), TIC1324 (SEQ ID NO:46), and TIC1407 (SEQ ID NO:50), each exhibited a score of 3 where as TIC1408 (SEQ ID NO:54) exhibited a score of 2.75. Proteins TIC1308 (SEQ ID NO: 58) and TIC1442 (SEQ ID NO: 60), each exhibited a score of 1. Proteins were expressed from a vegetative specific promoter and fed to insects by applying sporulated bacterial cells or culture supernatant to artificial insect diet. For polypeptides expressed from a sporulation specific promoter a 10-20x spore-crystal preparation with about 500-4000 ppm protein was applied to the insect diet. Stunting or mortality was observed on one or more of these insects: CEW (Corn Ear Worm); SCR (Southern corn Root worm); WCR (western corn root worm); ECB (European corn borer); WTPB (Western tarnished plant bug); TPB (Tarnished plant bug); FAW (Fall army worm); CPB (Colorado potato beetle). TIC1277 and TIC1311 were found to cause significant stunting of ECB and TIC1310 was found to cause significant stunting of WTPB and significant stunting and mortality of CPB.

Example 4

Transformed Plants

Nucleotide segments encoding TIC1506 (SEQ ID NO:11), TIC1503 (SEQ ID NO: 19), TIC614 (SEQ ID NO:3),

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TIC1324 (SEQ ID NO:27), TIC1407 (SEQ ID NO:31), TIC1408 (SEQ ID NO:35), are codon-optimized for plant expression and operably linked to one or more plant functional promoters and introduced into plant cells. Recombinant plants are regenerated from such transformed plant cells, and the regenerated plants are evaluated for resistance to pest infestation, such as insect tolerance and/or plant pathogenic nematode tolerance.

Nucleotide segments encoding ET34 (SEQ ID NO:3), 10 ET34+P139 secretion signal (SEQ ID NO:7), TIC1501 (SEQ ID NO:15), TIC615 (SEQ ID NO:7), TIC1277 (SEQ ID NO:11), TIC1278 (SEQ ID NO:15), TIC1310 (SEQ ID NO:19), TIC1311 (SEQ ID NO:23), TIC1308 (SEQ ID NO: 61), and TIC1442 (SEQ ID NO: 63) were codon-optimized 15 for plant expression and operably linked to one or more plant functional promoters and introduced into plant cells. Recombinant plants were regenerated from such transformed plant cells, and the regenerated plants were evaluated for resistance to pest infestation, such as insect tolerance and/or plant pathogenic nematode tolerance.

Example 5

Transformation of Soybean

This example describes a method of producing transgenic soybean plants and transgenic plant parts such as seeds. Other methods are known in the art of plant cell transformation that can be applied to transform plant cells and regenerate transgenic plants using the recombinant constructs of the invention. The methods of obtaining transgenic soybean plants and seeds are used as essentially disclosed in US Patent Application Publication Number US2009-0138985A1. Briefly, *Agrobacterium* containing a construct of Example 5 are grown in 30 Luria Burtani (LB) media containing spectinomycin at about 28° C. for over night. The bacterial culture is centrifuged, pellet washed, and resuspended in INO medium for inoculating wet or dry mature embryos explants. The explants are mixed with the *Agrobacterium* cell suspensions and briefly 35 exposed to sonication energy from a standard laboratory water bath cleaning sonicator. The explants are drained of any liquid and transferred to containers containing filter paper moistened with INO media and co-cultured in a lighted chamber at about 16 hours of light (≥ 5 uE) at about 23° to 28 C.° for 40 1 to 5 days. After co-culture, the explants are placed directly onto regeneration media containing a selective agent such as spectinomycin from about 7 to about 42 days. The cultures are 45 subsequently transferred to a media suitable for the recovery of transformed plantlets. Spectinomycin resistant shoots that have green buds or leaves are considered transformed and placed in soil or on a soil substitute for rooting in the presence 50 or absence of the selective agent. Progeny transgenic plants and seed are selected that provide pest resistance, especially nematode resistance.

Example 6

Testing of Transgenic Plant for Soybean Cyst Nematode (SCN) Resistance

An SCN pot assay was used to evaluate the resistance of transgenic soybean plants comprising one or more of the polynucleotide sequences of SEQ ID NOs: 3, 7, and 15 to infection by and reproduction of the SCN (*Heterodera glycines*) on roots. Three or four inch diameter square pots were 60 filled with clean sand and watered thoroughly. Transgenic and control soybean seeds, or alternatively any rooted plant parts,

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were planted one per pot in the center of the pot and watered well to remove air pockets. The pots were incubated in the greenhouse or growth chamber at 20° C. to 30° C. until the plants reached a suitable age for inoculation. Soybeans started from seed were typically inoculated 2-3 weeks after planting, while transplants were inoculated 1-3 days after planting. The test inoculum consisted of eggs from ripe *H. glycines* cysts collected from the soil and roots of infested soybean plants. An 80 micron mesh sieve was used to collect the cysts, which were then crushed in a Tenbroeck glass tissue homogenizer to release the eggs. The eggs were further purified by sieving and centrifugation over 40 percent sucrose solution at 4000 RPM for 5 minutes. Inoculum for an experiment consisted of water containing 500 vermiform eggs per mL. Five mL of the egg suspension was applied over the surface of the sand containing the test plants and the eggs were lightly watered in. The test plants were then returned to the greenhouse or growth chamber and incubated for 3-4 weeks to allow for root infection and cyst formation. The roots were then harvested. The severity of nematode infection was measured by counting the number of nematode cysts adhering to the root system.

Transgenic soybean plants comprising SEQ ID NO: 3 were tested in six different constructs, where in each construct SEQ ID NO: 3 was operably linked to a different promoter. Transgenic soybean plants comprising SEQ ID NO: 7 were tested in two different constructs, each construct having a different promoter. Transgenic soybean plants comprising SEQ ID NO: 15 were tested expressed from one construct.

Table 1 reports data illustrating plants from multiple events per multiple constructs that were evaluated for and determined to have significant cyst reduction against SCN when compared to the untransformed soybean cultivar. The number of plant roots tested was about equally distributed among the number of events tested.

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Plates were incubated at 23-25° C. with a 16 hour light/8 hour dark cycle for 7-10 days. BCN eggs were placed on the sterile filter paper and hatched in 5 mM ZnSO₄ solution for 5-7 days at 25° C. J2 stage juvenile nematodes were collected, rinsed in sterile water, and treated with 0.5% chlorhexidine diacetate for 10-15 minutes. Treated juvenile J2 nematodes were collected and rinsed twice in sterile water and stored in sterile water for infestation purposes.

For the infestation assay, about 10-15 *Arabidopsis* seeds were sprinkled on steamed sand in a pot and covered with a clear plastic dome. Several such dome/flat combos were placed in a flat and then covered with a black tray and transferred to a cold room for vernalization. On day 4, the flat was taken out of the cold room, the black tray is removed, and the flat was placed in a growth chamber for acclimating seeds at 26° C., 70% humidity, 140-180 µE light, 12 hours day length. The pots were watered and fertilized as needed. Three weeks after planting, the *Arabidopsis* plants were inoculated with 3,000 BCN eggs. About 35 days after inoculation the plants were harvested and cysts extracted by washing the plant's roots in a bucket of water and filtering the water through a 16 mesh sieve on top of a 50 mesh sieve. The cysts were collected off the top of the 50 mesh sieve and counted. Plants with lesser number of cysts compared to non-transgenic or transgenic control were considered resistant to BCN.

Table 2 reports data illustrating plants from multiple events per multiple constructs that were evaluated for and determined to have lesser number of BCN cysts compared to the untransformed *Arabidopsis* parental background. The number of plant roots tested was nearly equally distributed among the number of events tested.

TABLE 1

Severity of Soybean Cyst Nematode cyst infection on soybean plant roots					
Protein Name	SEQ ID NO:	Construct Name	Number of Events tested	Number of plant roots tested	Result (compared to control non-transgenic plants)
ET34	3	128213	14	177	1 of 14 events showed 35.4% cyst reduction
ET34	3	126168	15	389	7 of 15 events showed more than 46.7% cyst reduction
ET34	3	126626	15	191	0 of 15 events showed significant cyst reduction
ET34	3	126630	16	204	1 of 16 events showed 42.0% cyst reduction
ET34	3	127056	15	191	3 of 15 events showed more than 41.5% cyst reduction
ET34	3	128296	14	168	2 of 14 events showed more than 33% cyst reduction
P139 + ET34	7	126169	15	176	0 of 15 events showed the significant cyst reduction
P139 + ET34	7	126628	16	192	0 of 16 events showed the significant cyst reduction
TIC1501	15	133535	5	18	3 of 5 events showed more than 45% cyst reduction

Example 7

Testing of Transgenic *Arabidopsis* Plant for Beet Cyst Nematode (BCN) Resistance

Transgenic *Arabidopsis* seeds and plants comprising one or more of the polynucleotide sequences of SEQ ID NOs 3, 15, 27, 31, 35, 39, 43, 61, and 63 were produced by the method of Clough et al., 1998 (Plant J. 16:735-743) and tested for Beet Cyst Nematode (BCN) resistance by the method of Sijmons et al., 1991 (Plant J. 1: 245-254) and Vaghchhipawala et al., 2004 (Genome 47: 404-13).

Arabidopsis (variety Columbia-0) seeds were surface sterilized and rinsed with sterile water and plated on B5 medium.

TABLE 2

Severity of Beet Cyst Nematode cyst infection on <i>Arabidopsis thaliana</i> plant roots						
55	Protein Name	SEQ ID NO:	Construct Name	Number of Events tested	Number of plant roots tested	Resulting number of events having a lower mean cyst count compared to non-transgenic control
60	ET34	3	140057	6	72	3
	TIC1501	15	140056	6	72	3
	TIC615	27	139822	6	72	4
65	TIC1277	31	142259	6	71	2
	TIC1278	35	141647	6	72	4

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TABLE 2-continued

Severity of Beet Cyst Nematode cyst infection on <i>Arabidopsis thaliana</i> plant roots						
Protein Name	SEQ NO:	ID	Construct Name	Number of Events tested	Number of plant roots tested	Resulting number of events having a lower mean cyst count compared to non-transgenic control
TIC1310	39	142255		6	72	1
TIC1311	43	141644		6	71	6
TIC1308	61	141250		6	70	2
TIC1422	63	141205		6	72	2

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Various patent and non-patent publications are cited herein, the disclosures of each of which are incorporated herein by reference in their entirieties. Documents cited herein as being available from the World Wide Web at certain internet addresses are also incorporated herein by reference in their entirieties.

As various modifications could be made in the compositions and methods herein described and illustrated without departing from the scope of the invention, it is intended that all matter contained in the foregoing description or shown in the accompanying drawings shall be interpreted as illustrative rather than limiting. Thus, the breadth and scope of the present invention should not be limited by any of the above-described exemplary embodiments, but should be defined only in accordance with the following claims appended hereto and their equivalents.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 64

<210> SEQ ID NO 1

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 1

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<210> SEQ ID NO 2

<211> LENGTH: 126

<212> TYPE: PRT

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 2

Met	Thr	Val	Tyr	Asn	Ala	Thr	Phe	Thr	Ile	Asn	Phe	Tyr	Asn	Glu	Gly
1														15	

Glu	Trp	Gly	Gly	Pro	Glu	Pro	Tyr	Gly	Tyr	Ile	Lys	Ala	Tyr	Leu	Thr
20															30

Asn	Pro	Asp	His	Asp	Phe	Glu	Ile	Trp	Lys	Gln	Asp	Asp	Trp	Gly	Lys
35															45

Ser	Thr	Pro	Glu	Arg	Ser	Thr	Tyr	Thr	Gln	Thr	Ile	Lys	Ile	Ser	Ser
50															60

Asp	Thr	Gly	Ser	Pro	Ile	Asn	Gln	Met	Cys	Phe	Tyr	Gly	Asp	Val	Lys
65															80

Glu	Tyr	Asp	Val	Gly	Asn	Ala	Asp	Ile	Leu	Ala	Tyr	Pro	Ser	Gln	
85															95

Lys	Val	Cys	Ser	Thr	Pro	Gly	Val	Thr	Val	Arg	Leu	Asp	Gly	Asp	Glu
100															110

Lys	Gly	Ser	Tyr	Val	Thr	Ile	Lys	Tyr	Ser	Leu	Thr	Pro	Ala	
115														125

<210> SEQ ID NO 3

<211> LENGTH: 381

-continued

<212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: recombinant polynucleotide encoding an ET34 protein.

<400> SEQUENCE: 3

```

atgactgttt acaacgctac tttcaactatt aacttctaca acgagggtga gtgggggtgga      60
cctcgacccat acgggttacat taaggcttac ttgactaatac cagatcatga tttcgagatt     120
tggaaagcaag atgattgggg caagagcact ccagagcgct ctacctacac ccaaaccatt     180
aagatttcat ccgataccgg atcacccatc aatcagatgt gcttctacgg agatgttaag     240
gagtatgtat ttggcaatgc tgacgacatc cttgcctatc cttcccagaa ggtctgttagt     300
acacccggcg tcacagttag gctcgacggc gacgagaagg gttcctatgt aaccatcaag     360
tattcgctga cgcctgcatg a                                         381

```

<210> SEQ ID NO 4
 <211> LENGTH: 126
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID NO 3 from nucleotide position 1 through nucleotide position 378

<400> SEQUENCE: 4

```

Met Thr Val Tyr Asn Ala Thr Phe Thr Ile Asn Phe Tyr Asn Glu Gly
1           5           10          15

Glu Trp Gly Gly Pro Glu Pro Tyr Gly Tyr Ile Lys Ala Tyr Leu Thr
20          25          30

Asn Pro Asp His Asp Phe Glu Ile Trp Lys Gln Asp Asp Trp Gly Lys
35          40          45

Ser Thr Pro Glu Arg Ser Thr Tyr Thr Gln Thr Ile Lys Ile Ser Ser
50          55          60

Asp Thr Gly Ser Pro Ile Asn Gln Met Cys Phe Tyr Gly Asp Val Lys
65          70          75          80

Glu Tyr Asp Val Gly Asn Ala Asp Asp Ile Leu Ala Tyr Pro Ser Gln
85          90          95

Lys Val Cys Ser Thr Pro Gly Val Thr Val Arg Leu Asp Gly Asp Glu
100         105         110

Lys Gly Ser Tyr Val Thr Ile Lys Tyr Ser Leu Thr Pro Ala
115         120         125

```

<210> SEQ ID NO 5
 <211> LENGTH: 453
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: recombinant polynucleotide encoding a P139 secretion signal peptide (nucleotide position 1-75) fused in frame to a native Bt nucleotide sequence encoding a ET34 protein (nucleotide position 76-450)

<400> SEQUENCE: 5

```

atgaggagtt tcgcggctt gttgccgtt ctcgtcacct tctgcgtggt ggccgcctct      60
tccgacgccc ccaccacagt atataaacca actttcacca ttaatttcta taatgaaggaa     120
aatggggggg ggccagaacc atatggttat ataaaagcat atcttacaaa tccagatcat     180
gatttgaaa ttggaaaca agatgattgg gggaaaagta ctcctgagag aagtacttat     240
acggaaacca taaaaataad taacggacact cttccctta taaacccaaat gtgtttttat     300

```

-continued

```

ggtgatgtga aagaatacga cgtaggaaat gcagatgata ttctcgctta tccaaatcaa      360
aaagtatgcgtacacctgg tgtaacagta cgacttcatg gcatgagaa aggttcttat      420
gtgacaattt agtattcctt gactccagca taa                                453

```

```

<210> SEQ ID NO 6
<211> LENGTH: 150
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID
NO: 5.

```

<400> SEQUENCE: 6

```

Met Arg Ser Phe Ala Val Leu Leu Pro Leu Leu Val Thr Phe Cys Val
1           5           10          15

```

```

Val Ala Pro Pro Ser Asp Ala Ala Thr Thr Val Tyr Asn Ala Thr Phe
20          25          30

```

```

Thr Ile Asn Phe Tyr Asn Glu Gly Glu Trp Gly Gly Pro Glu Pro Tyr
35          40          45

```

```

Gly Tyr Ile Lys Ala Tyr Leu Thr Asn Pro Asp His Asp Phe Glu Ile
50          55          60

```

```

Trp Lys Gln Asp Asp Trp Gly Lys Ser Thr Pro Glu Arg Ser Thr Tyr
65          70          75          80

```

```

Thr Gln Thr Ile Lys Ile Ser Ser Asp Thr Gly Ser Pro Ile Asn Gln
85          90          95

```

```

Met Cys Phe Tyr Gly Asp Val Lys Glu Tyr Asp Val Gly Asn Ala Asp
100         105         110

```

```

Asp Ile Leu Ala Tyr Pro Ser Gln Lys Val Cys Ser Thr Pro Gly Val
115         120         125

```

```

Thr Val Arg Leu Asp Gly Asp Glu Lys Gly Ser Tyr Val Thr Ile Lys
130         135         140

```

```

Tyr Ser Leu Thr Pro Ala
145         150

```

```

<210> SEQ ID NO 7
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: a recombinant polynucleotide sequence encoding
a P139 secretion signal peptide (nucleotide position 1-75) fused
in frame to a synthetic nucleotide sequence encoding a ET34
protein (nucleotide position 76-450)

```

<400> SEQUENCE: 7

```

atgaggagtt tcgccccgtt gttgccgtt ctcgtcacct tctgcgttgt ggccctcct      60

```

```

tccgacgccc ccaccactgt ttacaacgct actttcaacta ttaacttcta caacgagggt     120

```

```

gagtggggtg gacctgagcc ttacggttac attaaggctt acttgactaa tccagatcat     180

```

```

gatttcgaga tttggaaagca agatgattgg ggcaagagca ctccagagcg ctctacctac     240

```

```

acccaaaccca ttaagatttc atccgatacc ggatcacccca tcaatcagat gtgcttctac     300

```

```

ggagatgtta aggagatgttga tggatggcaat gctgacgaca tccttgccata tccctccag     360

```

```

aaggctgttga gtacacccgg cggtcacagtg aggctcgacg gcgacgagaa gggttccat     420

```

```

gtaaccatca agtattcgct gacgcctgcga tga                                453

```

<210> SEQ ID NO 8

-continued

<211> LENGTH: 150
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID NO: 7.

<400> SEQUENCE: 8

Met	Arg	Ser	Phe	Ala	Val	Leu	Leu	Pro	Leu	Leu	Val	Thr	Phe	Cys	Val
1					5			10			15				

Val	Ala	Pro	Pro	Ser	Asp	Ala	Ala	Thr	Thr	Val	Tyr	Asn	Ala	Thr	Phe
	20					25				30					

Thr	Ile	Asn	Phe	Tyr	Asn	Glu	Gly	Glu	Trp	Gly	Gly	Pro	Glu	Pro	Tyr
	35				40				45						

Gly	Tyr	Ile	Lys	Ala	Tyr	Leu	Thr	Asn	Pro	Asp	His	Asp	Phe	Glu	Ile
	50					55			60						

Trp	Lys	Gln	Asp	Asp	Trp	Gly	Lys	Ser	Thr	Pro	Glu	Arg	Ser	Thr	Tyr
	65				70			75		80					

Thr	Gln	Thr	Ile	Lys	Ile	Ser	Ser	Asp	Thr	Gly	Ser	Pro	Ile	Asn	Gln
		85				90			95						

Met	Cys	Phe	Tyr	Asp	Val	Lys	Glu	Tyr	Asp	Val	Gly	Asn	Ala	Asp	
		100				105			110						

Asp	Ile	Leu	Ala	Tyr	Pro	Ser	Gln	Lys	Val	Cys	Ser	Thr	Pro	Gly	Val
	115				120			125							

Thr	Val	Arg	Leu	Asp	Gly	Asp	Glu	Lys	Gly	Ser	Tyr	Val	Thr	Ile	Lys
	130				135			140							

Tyr	Ser	Leu	Thr	Pro	Ala										
	145				150										

<210> SEQ ID NO 9
<211> LENGTH: 966
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 9

gcaataactc	catacgctga	atcttatatt	gatactgttc	aagatagaat	gaaacaaga	60
gatagggaat	caaaaactaac	tggtaaacca	ataaatatgc	aagaacaaat	aatagatgga	120
tggtttttag	ctagattctg	gatattttaa	gatcaaaata	acaatcatca	aacaaataga	180
tttataatcct	ggtttaaaga	taatcttgc	agttcgaagg	ggtatgacag	tatagcagaa	240
caaataatggct	taaaaataga	agcattaaat	gatatggatg	taacaaatata	tgattataca	300
tctaaaacag	gtgataccat	atataatgga	atttctgaac	taacaaatata	tacaggaaca	360
accaaaaaaaa	tgaaaaccga	tagtttcaa	agagattata	caaaatctga	atccacttca	420
gttaacaaatg	gttacaaatt	aggattttaa	gttgctgcta	agggagtagt	tgcattagca	480
ggtgccgatt	ttgaaaacaag	ttgttacctat	aatttatcat	ctactacaac	tgaaacaaat	540
acaatatacg	ataagtttac	ttgtccatct	caagaagtta	cattatcccc	aggacataaa	600
gcagttggta	aacatgattt	gagaaaaatg	gtgtattttg	ggactcatga	tttaaagggt	660
gattnaaag	taggtttaa	tgataaagag	attgtacaaa	aattttat	tccaaattat	720
agatcaattt	atttatctga	tattcgtaaa	acaatgattt	aaattgataa	atggaatcat	780
gttaataatcca	ttgactttta	tcaatttagtt	ggagttaaaa	atcatataaa	aatgggtat	840
actttatata	tagatacccc	ggccgaattt	acatthaatg	gagctaatcc	atattataga	900
gcaacattna	cagaatacga	cgagaacgga	aatcctgttc	aaacaaagat	tttaagtgga	960

-continued

aattaa

966

<210> SEQ ID NO 10
<211> LENGTH: 321
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID NO: 9.

<400> SEQUENCE: 10

Met	Ile	Thr	Pro	Tyr	Ala	Glu	Ser	Tyr	Ile	Asp	Thr	Val	Gln	Asp	Arg
1									5					15	

Met	Lys	Gln	Arg	Asp	Arg	Glu	Ser	Lys	Leu	Thr	Gly	Lys	Pro	Ile	Asn
									20				30		

Met	Gln	Glu	Gln	Ile	Ile	Asp	Gly	Trp	Phe	Leu	Ala	Arg	Phe	Trp	Ile
									35			45			

Phe	Lys	Asp	Gln	Asn	Asn	Asn	His	Gln	Thr	Asn	Arg	Phe	Ile	Ser	Trp
									50			55	60		

Phe	Lys	Asp	Asn	Leu	Ala	Ser	Ser	Lys	Gly	Tyr	Asp	Ser	Ile	Ala	Glu
								65	70		75		80		

Gln	Met	Gly	Leu	Lys	Ile	Glu	Ala	Leu	Asn	Asp	Met	Asp	Val	Thr	Asn
									85			90	95		

Ile	Asp	Tyr	Thr	Ser	Lys	Thr	Gly	Asp	Thr	Ile	Tyr	Asn	Gly	Ile	Ser
									100			105	110		

Glu	Leu	Thr	Asn	Tyr	Thr	Gly	Thr	Thr	Gln	Lys	Met	Lys	Thr	Asp	Ser
									115			120	125		

Phe	Gln	Arg	Asp	Tyr	Thr	Lys	Ser	Glu	Ser	Thr	Ser	Val	Thr	Asn	Gly
								130	135		140				

Leu	Gln	Leu	Gly	Phe	Lys	Val	Ala	Ala	Lys	Gly	Val	Val	Ala	Leu	Ala
								145	150		155		160		

Gly	Ala	Asp	Phe	Glu	Thr	Ser	Val	Thr	Tyr	Asn	Leu	Ser	Ser	Thr	Thr
								165	170		175				

Thr	Glu	Thr	Asn	Thr	Ile	Ser	Asp	Lys	Phe	Thr	Val	Pro	Ser	Gln	Glu
								180	185		190				

Val	Thr	Leu	Ser	Pro	Gly	His	Lys	Ala	Val	Val	Lys	His	Asp	Leu	Arg
								195	200		205				

Lys	Met	Val	Tyr	Phe	Gly	Thr	His	Asp	Leu	Lys	Gly	Asp	Leu	Lys	Val
								210	215		220				

Gly	Phe	Asn	Asp	Lys	Glu	Ile	Val	Gln	Lys	Phe	Ile	Tyr	Pro	Asn	Tyr
								225	230		235		240		

Arg	Ser	Ile	Asp	Leu	Ser	Asp	Ile	Arg	Lys	Thr	Met	Ile	Glu	Ile	Asp
								245	250		255				

Lys	Trp	Asn	His	Val	Asn	Thr	Ile	Asp	Phe	Tyr	Gln	Leu	Val	Gly	Val
								260	265		270				

Lys	Asn	His	Ile	Lys	Asn	Gly	Asp	Thr	Leu	Tyr	Ile	Asp	Thr	Pro	Ala
								275	280		285				

Glu	Phe	Thr	Phe	Asn	Gly	Ala	Asn	Pro	Tyr	Tyr	Arg	Ala	Thr	Phe	Thr
								290	295		300				

Glu	Tyr	Asp	Glu	Asn	Gly	Asn	Pro	Val	Gln	Thr	Lys	Ile	Leu	Ser	Gly
								305	310		315		320		

Asn

<210> SEQ ID NO 11
<211> LENGTH: 966
<212> TYPE: DNA

-continued

<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: recombinant polynucleotide encoding a TIC1506 protein.

<400> SEQUENCE: 11

atgattactc	cttacgctga	gtcttacatt	gatactgttc	aagatcgcat	gaagcaacgt	60
gatcgtgagt	ctaagttgac	tggcaaggct	attaacatgc	aagagcaaat	tatcgacggt	120
tggttccctag	ccagattctg	gatcttcaag	gatcagaaca	ataaccacca	gaccaaccgc	180
ttcatcagtt	ggttcaaggta	taacttggct	agttctaagg	gttacgatag	tattgctgag	240
caaatagggtt	tgaagattga	ggcttgaac	gatatggatg	ttaccaacat	tgattacact	300
tccaagactg	gtgatacgat	ctacaacggt	atttctgagt	tgactaacta	cactggtaact	360
actcagaaga	tgaagaccga	cagttccag	agggattaca	ccaagtctga	gtcaacacctca	420
gttaccaacg	gacttcagct	tggattcaag	gttgcagcca	agggagttgt	ggcacttgct	480
ggagcagatt	tcgagacctc	agttacctac	aacctttcat	ccaccacaaac	cgaaacgaac	540
accatctccg	ataagtttac	cgttccatcc	caggaagtga	cactttcccc	aggacacaag	600
gccgtggtca	agcacatct	caggaagatg	gtgtacttcg	gaacacacga	cctcaaaggc	660
gacctaag	tggggtttaa	cgacaaagaa	atcgtgcaga	agttcatcta	tccaaattat	720
cgcagcatcg	acctcagcga	catccgaaag	acaatgatcg	aaatcgacaa	atggaatcac	780
gtcaacacaa	tcgacttcta	tcaactggtc	ggcgtaaaga	accacatcaa	gaacggcgac	840
acactctaca	tcgacacacc	cgcgagttt	acattcaatg	gggcaatcc	ctattatcg	900
gcgacattca	cggaatacga	cgagaatggg	aatccggta	agacgaagat	cctgtcgaaa	960
aattga						966

<210> SEQ ID NO 12
<211> LENGTH: 321
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID NO: 11.

<400> SEQUENCE: 12

Met	Ile	Thr	Pro	Tyr	Ala	Glu	Ser	Tyr	Ile	Asp	Thr	Val	Gln	Asp	Arg
1									5						15

Met	Lys	Gln	Arg	Asp	Arg	Glu	Ser	Lys	Leu	Thr	Gly	Lys	Pro	Ile	Asn
									20						30

Met	Gln	Glu	Gln	Ile	Ile	Asp	Gly	Trp	Phe	Leu	Ala	Arg	Phe	Trp	Ile
									35						45

Phe	Lys	Asp	Gln	Asn	Asn	Asn	His	Gln	Thr	Asn	Arg	Phe	Ile	Ser	Trp
									50						60

Phe	Lys	Asp	Asn	Leu	Ala	Ser	Ser	Lys	Gly	Tyr	Asp	Ser	Ile	Ala	Glu
									65						80

Gln	Met	Gly	Leu	Lys	Ile	Glu	Ala	Leu	Asn	Asp	Met	Asp	Val	Thr	Asn
									85						95

Ile	Asp	Tyr	Thr	Ser	Lys	Thr	Gly	Asp	Thr	Ile	Tyr	Asn	Gly	Ile	Ser
									100						110

Glu	Leu	Thr	Asn	Tyr	Thr	Gly	Thr	Thr	Gln	Lys	Met	Lys	Thr	Asp	Ser
									115						125

Phe	Gln	Arg	Asp	Tyr	Thr	Lys	Ser	Glu	Ser	Thr	Ser	Val	Thr	Asn	Gly
									130						140

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38

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Leu Gln Leu Gly Phe Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala
 145 150 155 160
 Gly Ala Asp Phe Glu Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr
 165 170 175
 Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu
 180 185 190
 Val Thr Leu Ser Pro Gly His Lys Ala Val Val Lys His Asp Leu Arg
 195 200 205
 Lys Met Val Tyr Phe Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val
 210 215 220
 Gly Phe Asn Asp Lys Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr
 225 230 235 240
 Arg Ser Ile Asp Leu Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp
 245 250 255
 Lys Trp Asn His Val Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val
 260 265 270
 Lys Asn His Ile Lys Asn Gly Asp Thr Leu Tyr Ile Asp Thr Pro Ala
 275 280 285
 Glu Phe Thr Phe Asn Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr
 290 295 300
 Glu Tyr Asp Glu Asn Gly Asn Pro Val Gln Thr Lys Ile Leu Ser Gly
 305 310 315 320

Asn

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<210> SEQ ID NO 13
<211> LENGTH: 681
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 13

gcaataactc catatgctga atcttatatt gatactgttc aagatagaat gaaacaaga 60
gataggaaat caaaactaac tggtaaacca ataaatatgc aagaacaat aatagatgga 120
tggtttttag ctagattctg gatattttaa gatcaaataa acaatcatca aacaaataga 180
tttatatcct ggttaaaga taatcttgct agttcgagg ggtatgacag tatagcagaa 240
caaataggct taaaataga agcattaaat gatatggatg taacaaatata tgattataca 300
tctaaaacag gtgataccat atataatgga atttctgaac taacaaatata tacaggaaca 360
accaaaaaaaaa tgaaaaaccga tagtttcaa agagattata caaaatctga atccacttca 420
gtaacaaatg ggttacaatt aggattttaa gttgctgcta agggagtagt tgcattagca 480
ggtgcagatt ttgaaacaag tggcacatct aatttatcat ctactacaac tggaaacaaat 540
acaatatacg ATAAGTTAC TGTCCATCT caagaagtta cattatcccc aggacataaa 600
gcagtgggtga aacatgattt gagaaaaatg gtgtatTTG ggactcatga tttaaaggt 660
gatttaaaag taggttttaa t 681
  
```

```

<210> SEQ ID NO 14
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID
NO: 13.

<400> SEQUENCE: 14
  
```

Met Ile Thr Pro Tyr Ala Glu Ser Tyr Ile Asp Thr Val Gln Asp Arg

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39**40**

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1	5	10	15
Met Lys Gln Arg Asp Arg Glu Ser Lys Leu Thr Gly Lys Pro Ile Asn			
20	25	30	
Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile			
35	40	45	
Phe Lys Asp Gln Asn Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp			
50	55	60	
Phe Lys Asp Asn Leu Ala Ser Ser Lys Gly Tyr Asp Ser Ile Ala Glu			
65	70	75	80
Gln Met Gly Leu Lys Ile Glu Ala Leu Asn Asp Met Asp Val Thr Asn			
85	90	95	
Ile Asp Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser			
100	105	110	
Glu Leu Thr Asn Tyr Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser			
115	120	125	
Phe Gln Arg Asp Tyr Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly			
130	135	140	
Leu Gln Leu Gly Phe Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala			
145	150	155	160
Gly Ala Asp Phe Glu Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr			
165	170	175	
Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu			
180	185	190	
Val Thr Leu Ser Pro Gly His Lys Ala Val Val Lys His Asp Leu Arg			
195	200	205	
Lys Met Val Tyr Phe Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val			
210	215	220	
Gly Phe Asn			
225			

<210> SEQ ID NO 15
<211> LENGTH: 684
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: a recombinant polynucleotide sequence encoding
a TIC1501 protein.

<400> SEQUENCE: 15

atgattactc cttacgctga gtcttacatt gatactgttc aagatcgcat gaagcaacgt	60
gatcgtgagt ctaagttgac tggcaagcct attaacatgc aagagcaaat tatcgacggt	120
tggttccctag ccagattctg gatcttcaag gatcagaaca ataaccacca gaccaaccgc	180
ttccatcgtt ggttcaagga taacctggct agttctaagg gttacgatag tattgctgag	240
caaatagggtt tgaagattga ggcttgaac gatatggatg ttaccaacat tgattacact	300
tccaagactg gtgatacgtat ctacaacggat atttctgagt tgactaacta cactggtact	360
actcagaaga tgaagaccga cagcttccag agggattaca ccaagtctga gtcaacctca	420
gttaccaacg gacttcagct tggattcaag gttgcagccaa agggagttgt ggcacttgct	480
ggagcagatt tcgagacactc agttacccatc aacctttcat ccaccacaaac cgaaacgaaac	540
accatctccg ataagtttac cggtccatcc caggaagtga cactttcccc aggacacaag	600
gccgtggtca agcacgatct caggaagatg gtgtacttcg gaacacacgca cctcaaaggc	660
gacactcaaag tgggctttaa ctga	684

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<210> SEQ ID NO 16
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID NO: 15.

<400> SEQUENCE: 16

Met	Ile	Thr	Pro	Tyr	Ala	Glu	Ser	Tyr	Ile	Asp	Thr	Val	Gln	Asp	Arg
1									5		10		15		

Met	Lys	Gln	Arg	Asp	Arg	Glu	Ser	Lys	Leu	Thr	Gly	Lys	Pro	Ile	Asn
									20		25		30		

Met	Gln	Glu	Gln	Ile	Ile	Asp	Gly	Trp	Phe	Leu	Ala	Arg	Phe	Trp	Ile
									35		40		45		

Phe	Lys	Asp	Gln	Asn	Asn	Asn	His	Gln	Thr	Asn	Arg	Phe	Ile	Ser	Trp
								50		55		60			

Phe	Lys	Asp	Asn	Leu	Ala	Ser	Ser	Lys	Gly	Tyr	Asp	Ser	Ile	Ala	Glu
								65		70		75		80	

Gln	Met	Gly	Leu	Lys	Ile	Glu	Ala	Leu	Asn	Asp	Met	Asp	Val	Thr	Asn
								85		90		95			

Ile	Asp	Tyr	Thr	Ser	Lys	Thr	Gly	Asp	Thr	Ile	Tyr	Asn	Gly	Ile	Ser
								100		105		110			

Glu	Leu	Thr	Asn	Tyr	Thr	Gly	Thr	Thr	Gln	Lys	Met	Lys	Thr	Asp	Ser
								115		120		125			

Phe	Gln	Arg	Asp	Tyr	Thr	Lys	Ser	Glu	Ser	Thr	Ser	Val	Thr	Asn	Gly
								130		135		140			

Leu	Gln	Leu	Gly	Phe	Lys	Val	Ala	Ala	Lys	Gly	Val	Val	Ala	Leu	Ala
								145		150		155		160	

Gly	Ala	Asp	Phe	Glu	Thr	Ser	Val	Thr	Tyr	Asn	Leu	Ser	Ser	Thr	Thr
								165		170		175			

Thr	Glu	Thr	Asn	Thr	Ile	Ser	Asp	Lys	Phe	Thr	Val	Pro	Ser	Gln	Glu
								180		185		190			

Val	Thr	Leu	Ser	Pro	Gly	His	Lys	Ala	Val	Val	Lys	His	Asp	Leu	Arg
								195		200		205			

Lys	Met	Val	Tyr	Phe	Gly	Thr	His	Asp	Leu	Lys	Gly	Asp	Leu	Lys	Val
								210		215		220			

Gly	Phe	Asn
		225

<210> SEQ ID NO 17
<211> LENGTH: 903
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 17

gcaataactc	catatgtca	atcttatatt	gatactgttc	aagatagaat	gaaacaaga	60
gatagggaat	caaaaactaac	tggtaaacca	ataaaatatgc	aagaacaaat	aatagatgg	120
tggtttttag	ctagattctg	gatatttaaa	gatcaaataa	acaatcatca	aacaaataga	180
tttataatcct	ggtttaaaga	taatcttgct	agttcgaagg	ggtatgacag	tatagcagaa	240
caaatgggct	taaaaaataga	agcattaaat	gatatggatg	taacaaatat	tgattataca	300
tctaaaacac	gtgataccat	ataataatgg	atttctgAAC	taacaaatTTA	tacaggaaca	360
accaaaaaaa	tgaaaaccga	tagtttcaa	agagattata	caaaatctga	atccacttca	420
gtaacaaaat	ggttacaatt	aggatttaaa	gttgctgcta	agggagtagt	tgcattagca	480

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```

ggtcgcagg ttgaaacaag ttttacccat aatttatcat ctactacaac tgaaacaaat      540
acaatatccg ataagtttac tttccatct caagaagtta cattatcccc aggacataaa      600
gcagtggta aacatgattt gaaaaatg gtgtatttg ggactcatga tttaaagggt      660
gatttaaaag taggtttaa tgataaagag attgtacaaa aatttattt tccaaattat      720
agatcaattt atttatctga tattcgtaaa acaatgattt aaattgataa atgaaatcat      780
gttaataccca ttgacttta tcaatttagtt ggagttaaaa atcatataa aaatggtgat      840
actttatata tagatacccc ggccgaattt acatthaatg gagctaattc atattataga      900
gca                                              903

```

```

<210> SEQ ID NO 18
<211> LENGTH: 301
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID
NO: 17.

```

<400> SEQUENCE: 18

```

Met Ile Thr Pro Tyr Ala Glu Ser Tyr Ile Asp Thr Val Gln Asp Arg
1           5          10          15

```

```

Met Lys Gln Arg Asp Arg Glu Ser Lys Leu Thr Gly Lys Pro Ile Asn
20          25          30

```

```

Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile
35          40          45

```

```

Phe Lys Asp Gln Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp
50          55          60

```

```

Phe Lys Asp Asn Leu Ala Ser Ser Lys Gly Tyr Asp Ser Ile Ala Glu
65          70          75          80

```

```

Gln Met Gly Leu Lys Ile Glu Ala Leu Asn Asp Met Asp Val Thr Asn
85          90          95

```

```

Ile Asp Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser
100         105         110

```

```

Glu Leu Thr Asn Tyr Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser
115         120         125

```

```

Phe Gln Arg Asp Tyr Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly
130         135         140

```

```

Leu Gln Leu Gly Phe Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala
145         150         155         160

```

```

Gly Ala Asp Phe Glu Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr
165         170         175

```

```

Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu
180         185         190

```

```

Val Thr Leu Ser Pro Gly His Lys Ala Val Val Lys His Asp Leu Arg
195         200         205

```

```

Lys Met Val Tyr Phe Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val
210         215         220

```

```

Gly Phe Asn Asp Lys Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr
225         230         235         240

```

```

Arg Ser Ile Asp Leu Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp
245         250         255

```

```

Lys Trp Asn His Val Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val
260         265         270

```

-continued

Lys	Asn	His	Ile	Lys	Asn	Gly	Asp	Thr	Leu	Tyr	Ile	Asp	Thr	Pro	Ala
275						280					285				

Glu	Phe	Thr	Phe	Asn	Gly	Ala	Asn	Pro	Tyr	Tyr	Arg	Ala		
290						295					300			

<210> SEQ ID NO 19

<211> LENGTH: 906

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: a recombinant polynucleotide sequence encoding a TIC1503 protein.

<400> SEQUENCE: 19

atgattactc	cttacgctga	gtcttacatt	gatactgttc	aagatgcgt	gaagcaacgt	60
gatcgtagt	ctaaggtagc	tggcaaggct	attaacatgc	aagagcaa	at tgcacgg	120
tggttccctag	ccagattctg	gatcttcaag	gatcagaaca	ataaccacca	gaccaacccgc	180
ttcatcgtt	ggttcaagga	taaattggct	agttctaaagg	gttacgatag	tattgctgag	240
caaattgggtt	tgaagattga	ggctttgaac	gatatggatg	ttaccaacat	tgattacact	300
tccaagactg	gtgatacgat	ctacaacgg	atttctgag	tgactaacta	cactggta	360
actcagaaga	tgaagaccga	cagttccag	agggattaca	ccaaagtctga	gtcaacctca	420
gttaccaacg	gacttcagct	tggattcaag	gttgcagcc	agggagttgt	ggcacttgct	480
ggagcagatt	tcgagacctc	agttacctac	aaccttcat	ccaccacaac	cggaaacgaa	540
accatctccg	ataaggta	cgttccatcc	caggaagtga	cacttcccc	aggacacaag	600
gccgtggta	agcacatct	caggaagatg	gtgtacttcg	gaacacacga	cctcaaaggc	660
gacctaag	tgggcttaa	cgacaaagaa	atcgtgcaga	agttcatcta	tccaaattat	720
cgcagcatcg	acctcagcga	catccgaaag	acaatgatcg	aaatcgacaa	atgaaatcac	780
gtcaacacaa	tcgacttcta	tcaactggc	ggcgtaaaga	accacatcaa	gaacggcgac	840
acactctaca	tcgacacacc	cggcgagtt	acattcaatg	ggccaaatcc	ctattatcg	900
gcgtga						906

<210> SEQ ID NO 20

<211> LENGTH: 301

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID NO: 19.

<400> SEQUENCE: 20

Met	Ile	Thr	Pro	Tyr	Ala	Glu	Ser	Tyr	Ile	Asp	Thr	Val	Gln	Asp	Arg
1						5			10				15		

Met	Lys	Gln	Arg	Asp	Arg	Glu	Ser	Lys	Leu	Thr	Gly	Lys	Pro	Ile	Asn
	20					25						30			

Met	Gln	Glu	Gln	Ile	Ile	Asp	Gly	Trp	Phe	Leu	Ala	Arg	Phe	Trp	Ile
	35					40						45			

Phe	Lys	Asp	Gln	Gln	Asn	Asn	Asn	His	Gln	Thr	Asn	Arg	Phe	Ile	Ser	Trp
	50					55			60							

Phe	Lys	Asp	Asn	Leu	Ala	Ser	Ser	Lys	Gly	Tyr	Asp	Ser	Ile	Ala	Glu
	65					70			75			80			

Gln	Met	Gly	Leu	Lys	Ile	Glu	Ala	Leu	Asn	Asp	Met	Asp	Val	Thr	Asn
	85					90							95		

Ile Asp Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser

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48

100	105	110
Glu Leu Thr Asn Tyr Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser		
115	120	125
Phe Gln Arg Asp Tyr Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly		
130	135	140
Leu Gln Leu Gly Phe Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala		
145	150	155
Gly Ala Asp Phe Glu Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr		
165	170	175
Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu		
180	185	190
Val Thr Leu Ser Pro Gly His Lys Ala Val Val Lys His Asp Leu Arg		
195	200	205
Lys Met Val Tyr Phe Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val		
210	215	220
Gly Phe Asn Asp Lys Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr		
225	230	235
Arg Ser Ile Asp Leu Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp		
245	250	255
Lys Trp Asn His Val Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val		
260	265	270
Lys Asn His Ile Lys Asn Gly Asp Thr Leu Tyr Ile Asp Thr Pro Ala		
275	280	285
Glu Phe Thr Phe Asn Gly Ala Asn Pro Tyr Tyr Arg Ala		
290	295	300

<210> SEQ ID NO 21
<211> LENGTH: 774
<212> TYPE: DNA
<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 21

```

atggacattc aagatgtaat agaattaatt agtgactatg ccaacaagtg gaagggacaa   60
caaaaatggaa gtcgttgta catgaaattc attgtatgcac gctttgcgaa caatgcatta 120
aaagtagaaag ctgatcgta tatgtacctg gagcctacag agcaagatata gccagatgt 180
aaatttagata cccaaatgttt taccaataact tccacacacg cccaaaactgtt ccagtttgat 240
atgtttggag aatacgatac ttggcaaaca tggagaatcg aagatggtgc aacagaagca 300
ggaaaaatgtc gctttccat tgagccattt ttttagatcg aggatgtttc tagtccacta 360
tctttatccc taaacgacac acttaccctc tcaggaaaaa agccatccc cggtgagggt 420
cgtgatcccc cagttcgacc acgtttcaaa gtaacgggtt cactcatggc aaaacccaaa 480
acatcaaccc gtgttttga cgtaaaacgt gacgtcacag gatatgtggg acttgcacaa 540
acttttagcat cccggagaact gcaagaatcg ttacacaatg tggcgctat tttccaacaa 600
tattatagtc cctatatcga agtaaatggt ggaagagtga catttcatga tcgtggtaa 660
tatcaatcat tagatgtaaag cagcatctat attcatattt ttgcagagag ctttagatatt 720
cccggtttaa cggaggtata taatattttt gacctaagca atggacgggtt ataa 774

```

<210> SEQ ID NO 22
<211> LENGTH: 257
<212> TYPE: PRT
<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 22

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-continued

Met Asp Ile Gln Asp Val Ile Glu Leu Ile Ser Asp Tyr Ala Asn Lys
 1 5 10 15

Trp Lys Glu Gln Gln Asn Gly Ser Arg Ser Asp Met Lys Phe Ile Asp
 20 25 30

Ala Arg Phe Ala Asn Asn Ala Leu Lys Val Glu Ala Asp Arg Thr Met
 35 40 45

Tyr Leu Glu Pro Thr Glu Gln Asp Met Pro Asp Val Lys Leu Asp Thr
 50 55 60

Gln Val Phe Thr Asn Thr Ser Thr Gln Pro Lys Thr Val Gln Phe Asp
 65 70 75 80

Met Phe Gly Glu Tyr Asp Thr Trp Gln Thr Trp Arg Ile Glu Asp Gly
 85 90 95

Ala Thr Glu Ala Gly Lys Cys Arg Phe Ala Ile Glu Pro Leu Phe Arg
 100 105 110

Ser Glu Asp Val Ser Ser Pro Leu Ser Leu Phe Leu Asn Asp Thr Leu
 115 120 125

Thr Leu Ser Gly Lys Lys Pro Phe Ser Val Glu Gly Arg Asp Phe Thr
 130 135 140

Val Arg Pro Arg Phe Lys Val Thr Gly Thr Leu Met Ala Lys Pro Lys
 145 150 155 160

Thr Ser Thr Arg Ala Phe Asp Val Lys Arg Asp Val Thr Gly Tyr Val
 165 170 175

Gly Leu Val Thr Thr Leu Ala Ser Gly Glu Leu Gln Glu Ser Leu His
 180 185 190

Asn Val Gly Ala Ile Phe Gln Gln Tyr Tyr Ser Pro Tyr Ile Glu Val
 195 200 205

Asn Gly Gly Arg Val Thr Phe His Asp Arg Gly Glu Tyr Gln Ser Leu
 210 215 220

Asp Val Ser Ser Ile Tyr Ile His Ile Phe Ala Glu Ser Leu Asp Ile
 225 230 235 240

Pro Gly Leu Thr Glu Glu Tyr Asn Ile Tyr Asp Leu Ser Asn Gly Arg
 245 250 255

Val

<210> SEQ ID NO 23
 <211> LENGTH: 774
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 23

```

atggacattc aagatgtgat tgagttgatt tctgattacg ccaacaagtg gaaggagcaa 60
cagaacggta gtcgttgta catgaagttc attgatgctc gttcgccaa caacgcttg 120
aagggttggg ctgatgcac tatgtaccta gggctactg agcaagacat gcctgtatgtt 180
aagttggata ctcaagtgtt cacgaacacc agtacccaac ctaagactgt tcagttcgac 240
atgttcgggt agtacgatac ctggcagacc tggagaattg aggtatgggc taccgaggcg 300
ggcaagtgc gattcgcaat tgagccattg ttccgctctg aggtatgttc ttccaccatt 360
tctctttcc ttaatgacac ccttaccctt tctggtaaga aaccattcag cggtgaagga 420
agggacttta ccgtgaggcc aaggttaaa gtgaccggaa cactcatggc caaacccaag 480
acttcaaccc gtgccttga cgtgaaacgc gacgtgacag gatacgtggg actcgtgaca 540

```

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51**52**

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```

acgctcgctt caggagaact ccaggaatca ctgcacaatg tcgggtccat ctttcagcag    600
tactacagcc cctacatcga agtcaatggc gggcgcgta cattccatga ccgaggcag    660
tatcagtccc tagacgtatc cagcatctac atccacatct ttgcggaaag cctcgacata    720
cctgggctca cggaggagta caacatctac gacctgtcga atgggggggt atga        774

```

<210> SEQ ID NO 24

<211> LENGTH: 257

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 24

```

Met Asp Ile Gln Asp Val Ile Glu Leu Ile Ser Asp Tyr Ala Asn Lys
1           5           10          15

```

```

Trp Lys Glu Gln Gln Asn Gly Ser Arg Ser Asp Met Lys Phe Ile Asp
20          25          30

```

```

Ala Arg Phe Ala Asn Asn Ala Leu Lys Val Glu Ala Asp Arg Thr Met
35          40          45

```

```

Tyr Leu Glu Pro Thr Glu Gln Asp Met Pro Asp Val Lys Leu Asp Thr
50          55          60

```

```

Gln Val Phe Thr Asn Thr Ser Thr Gln Pro Lys Thr Val Gln Phe Asp
65          70          75          80

```

```

Met Phe Gly Glu Tyr Asp Thr Trp Gln Thr Trp Arg Ile Glu Asp Gly
85          90          95

```

```

Ala Thr Glu Ala Gly Lys Cys Arg Phe Ala Ile Glu Pro Leu Phe Arg
100         105         110

```

```

Ser Glu Asp Val Ser Ser Pro Leu Ser Leu Phe Leu Asn Asp Thr Leu
115         120         125

```

```

Thr Leu Ser Gly Lys Pro Phe Ser Val Glu Gly Arg Asp Phe Thr
130         135         140

```

```

Val Arg Pro Arg Phe Lys Val Thr Gly Thr Leu Met Ala Lys Pro Lys
145         150         155         160

```

```

Thr Ser Thr Arg Ala Phe Asp Val Lys Arg Asp Val Thr Gly Tyr Val
165         170         175

```

```

Gly Leu Val Thr Thr Leu Ala Ser Gly Glu Leu Gln Glu Ser Leu His
180         185         190

```

```

Asn Val Gly Ala Ile Phe Gln Gln Tyr Tyr Ser Pro Tyr Ile Glu Val
195         200         205

```

```

Asn Gly Gly Arg Val Thr Phe His Asp Arg Gly Glu Tyr Gln Ser Leu
210         215         220

```

```

Asp Val Ser Ser Ile Tyr Ile His Ile Phe Ala Glu Ser Leu Asp Ile
225         230         235         240

```

```

Pro Gly Leu Thr Glu Glu Tyr Asn Ile Tyr Asp Leu Ser Asn Gly Arg
245         250         255

```

Val

```

<210> SEQ ID NO 25
<211> LENGTH: 900
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

```

<400> SEQUENCE: 25

```

atggctattt ttaattttga cgcaaaagta gtagagtttta ttaattggtg gacagcagag    60
ttcggtggca aagatcccag aaatattcaa attggttatg agaatcgaga catcaatgtt   120

```

-continued

gttccatcat caagtaaccc tagtgtcaat gtaataccta agtttagcaag atcatctgtt	180
caagaattgc aaaataatac aagtgttaacg cagacacaag agctggcatt ttcagaaaact	240
acaactgaaa gtcagtccttc tacaacaaca catggggctt cattttctac aacggtcacc	300
tctgttacgc aatttacagc tgaagttaat ttcaaagcga ttggttccctc aattgagcaa	360
actatcggcg tttctatgac aggagattat aattacagtt cttcactaac aaaaacaaca	420
gaaaagaga gatcttgac tctcacacaa ccggtagttg tcccacctt ttcacgtgta	480
acttgcacat tattgatata taatgcacca tttcagttac ctgtggactt aaattgtaat	540
gtattcggta cacttggcgg agatttttta gctagctaca cttacactgt tatttagtact	600
ggtcgaacag taaatactag tataactgct agtcaaatga ctcttacctc ttggccaggt	660
aaaccatctg aaattattgg tatcgacca aagcatggac ttattttaa agggacaggt	720
acacaggctg cagttacatgg attatactca accgttaat ttgttgaatc cccattgcc	780
ggtcaccaag gagaaaaaaag aacgttattac ctccagcgc aacctgtaaa tgaagatgat	840
ctgatttctt ctgtattnag taacattcca attattaatc ctgtttctaa tctataatga	900

<210> SEQ ID NO 26

<211> LENGTH: 298

<212> TYPE: PRT

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 26

Met Ala Ile Phe Asn Phe Asp Ala Lys Val Val Glu Phe Ile Asn Trp			
1	5	10	15

Trp Thr Ala Glu Phe Gly Gly Lys Asp Pro Arg Asn Ile Gln Ile Gly			
20	25	30	

Tyr Glu Asn Arg Asp Ile Asn Val Val Pro Ser Ser Ser Asn Pro Ser			
35	40	45	

Val Asn Val Ile Pro Lys Leu Ala Arg Ser Ser Val Gln Glu Leu Gln			
50	55	60	

Asn Asn Thr Ser Val Thr Gln Thr Gln Glu Leu Ala Phe Ser Glu Thr			
65	70	75	80

Thr Thr Glu Ser Gln Ser Ser Thr Thr His Gly Ala Ser Phe Ser			
85	90	95	

Thr Thr Val Thr Ser Val Thr Gln Phe Thr Ala Glu Val Asn Phe Lys			
100	105	110	

Ala Ile Gly Ser Ser Ile Glu Gln Thr Ile Gly Val Ser Met Thr Gly			
115	120	125	

Asp Tyr Asn Tyr Ser Ser Ser Leu Thr Lys Thr Thr Glu Lys Ser Arg			
130	135	140	

Ser Trp Thr Leu Thr Gln Pro Val Val Pro Pro Phe Ser Arg Val			
145	150	155	160

Thr Cys Thr Leu Leu Ile Tyr Asn Ala Pro Phe Ser Val Pro Val Asp			
165	170	175	

Leu Asn Cys Asn Val Phe Gly Thr Leu Gly Gly Asp Phe Leu Ala Ser			
180	185	190	

Tyr Thr Tyr Thr Val Ile Ser Thr Gly Arg Thr Val Asn Thr Ser Ile			
195	200	205	

Thr Ala Ser Gln Met Thr Leu Thr Ser Trp Pro Gly Lys Pro Ser Glu			
210	215	220	

Ile Ile Gly Ile Ala Pro Lys His Gly Leu Ile Phe Lys Gly Thr Gly			
225	230	235	240

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Thr Gln Ala Ala Val His Gly Leu Tyr Ser Thr Val Lys Phe Val Glu
245 250 255

Ser Pro Leu Pro Gly His Gln Gly Glu Lys Arg Thr Tyr Tyr Leu Pro
260 265 270

Ala Gln Pro Val Asn Glu Asp Asp Leu Ile Ser Ser Val Phe Ser Asn
275 280 285

Ile Pro Ile Ile Asn Pro Val Ser Asn Leu
290 295

<210> SEQ ID NO 27
<211> LENGTH: 897
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 27

atggcttatct tcaacttcga cgccaagggtg gtcgagttca tcaactggtg gactgctgag	60
ttcggccggca aagatccaag gaacatccag atcggctacg agaatcgtga catcaacgtg	120
gtcccttagct ctagecaaccc tagcgtgaat gtatcccga agctcgctag gtccagcgtta	180
caggaggttc agaacaacac cagcgttacc cagactcagg agctggcatt ctccgaaacg	240
acaacccaaat ccacgtccctc tactaccact cacggcgcatt ctttagcac taccgtgacc	300
tcagtgaccc aattcaccgc cgaggtcaac ttcaaggcaa tcggtagctc tattgagcaa	360
acaatcgccg tgagcatgac aggccattac aactactctt cttcgttgac caagacaacc	420
gagaaatcac gtcctggac gctgacgcag cctgttgtgg ttccctccctt ctctcgctc	480
acgtgcaccc tcataatcta caacgcgcc ttcagtgttc cagtcgatct caattgcaac	540
gtcttcggaa cgcttggagg cgactttctg gcctcgtaca cttacaccgt gatctcaacg	600
ggagaagaactg tcaacaccc tattaccgcg tctcagatga ctctcaccag ttggcctggg	660
aagccccatgt agatcattgg tatcgctccg aagcacggcc tcatacttcaa gggcactgggt	720
acacaggccg ccgtccacgg gttgtactca acggtaagt tcgttgaatc gccgcctccct	780
ggccatcagg gcgagaaacg gacctactat ctgccagcac aaccagtgaa cgaggacgat	840
cttatttcctt cgggtttctc caacattccg atcatcaacc cagtgccaa tctgtga	897

<210> SEQ ID NO 28
<211> LENGTH: 298
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 28

Met Ala Ile Phe Asn Phe Asp Ala Lys Val Val Glu Phe Ile Asn Trp	
1 5 10 15	
Trp Thr Ala Glu Phe Gly Gly Lys Asp Pro Arg Asn Ile Gln Ile Gly	
20 25 30	
Tyr Glu Asn Arg Asp Ile Asn Val Val Pro Ser Ser Ser Asn Pro Ser	
35 40 45	
Val Asn Val Ile Pro Lys Leu Ala Arg Ser Ser Val Gln Glu Leu Gln	
50 55 60	
Asn Asn Thr Ser Val Thr Gln Thr Gln Glu Leu Ala Phe Ser Glu Thr	
65 70 75 80	
Thr Thr Glu Ser Gln Ser Ser Thr Thr His Gly Ala Ser Phe Ser	

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58

85	90	95
Thr Thr Val Thr Ser Val Thr Gln Phe Thr Ala Glu Val Asn Phe Lys		
100	105	110
Ala Ile Gly Ser Ser Ile Glu Gln Thr Ile Gly Val Ser Met Thr Gly		
115	120	125
Asp Tyr Asn Tyr Ser Ser Ser Leu Thr Lys Thr Thr Glu Lys Ser Arg		
130	135	140
Ser Trp Thr Leu Thr Gln Pro Val Val Val Pro Pro Phe Ser Arg Val		
145	150	155
160		
Thr Cys Thr Leu Leu Ile Tyr Asn Ala Pro Phe Ser Val Pro Val Asp		
165	170	175
Leu Asn Cys Asn Val Phe Gly Thr Leu Gly Gly Asp Phe Leu Ala Ser		
180	185	190
Tyr Thr Tyr Thr Val Ile Ser Thr Gly Arg Thr Val Asn Thr Ser Ile		
195	200	205
Thr Ala Ser Gln Met Thr Leu Thr Ser Trp Pro Gly Lys Pro Ser Glu		
210	215	220
Ile Ile Gly Ile Ala Pro Lys His Gly Leu Ile Phe Lys Gly Thr Gly		
225	230	235
240		
Thr Gln Ala Ala Val His Gly Leu Tyr Ser Thr Val Lys Phe Val Glu		
245	250	255
Ser Pro Leu Pro Gly His Gln Gly Glu Lys Arg Thr Tyr Tyr Leu Pro		
260	265	270
Ala Gln Pro Val Asn Glu Asp Asp Leu Ile Ser Ser Val Phe Ser Asn		
275	280	285
Ile Pro Ile Ile Asn Pro Val Ser Asn Leu		
290	295	

<210> SEQ ID NO 29
<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 29

atgggaattt tcaacattttca agacgaaattt aatgactaca tgaaaaggat ttatggtgca	60
acatctgtta aaagcacata tgaccctca ttcaaaggat ttacacgatc tgtaacacct	120
caatatgtat tgatttcaac agaacctgtt aataatcata ttactactaa agcaataaat	180
aatccagcgt ctccagaagt aaccagtaca gtaaccttc catggacgga aaccgacact	240
gttaacctctg cagtgtactaa agggtataaa gtcgggttgtt cagtaagctc aaaagcaact	300
tttaaatttg cttttgttac ttctgtatgtt actgttaactg tatcagcaga atataattat	360
agtacaacaatg atacaacaac aaaaacagat acacgcacat ggacggatc gacgacagta	420
aaagccccctc caagaactaa tgttagaagtt gcatatatta tccaaactgg aaattataac	480
gttccgggtta atgttagatgc tgatatgtact ggaacgctat ttgcagagg gtatagagat	540
ggtgcaactaa ttgcagcgac ttatatttct ataacagatt tagcagatca caagcctaatt	600
ttgggtttaa caaataaagg ggtatgggtt gctcatttttta aagggtgaagg ttatataagag	660
ggtgcaacaag gcttaagaag ctatattca gttacagaat atccaatgga tgataaagac	720
agacgttcga cacaaaaaac ttatataattt gaagggttcat tagcacccaa tgttacttta	780
ataaatgata gaaaggaagg tagataaa	807

<210> SEQ ID NO 30

US 9,328,356 B2

59

60

-continued

<211> LENGTH: 268
 <212> TYPE: PRT
 <213> ORGANISM: Bacillus thuringiensis

 <400> SEQUENCE: 30

Met	Gly	Ile	Ile	Asn	Ile	Gln	Asp	Glu	Ile	Asn	Asp	Tyr	Met	Lys	Gly
1						5				10					15
Met	Tyr	Gly	Ala	Thr	Ser	Val	Lys	Ser	Thr	Tyr	Asp	Pro	Ser	Phe	Lys
	20							25						30	
Val	Phe	Asn	Glu	Ser	Val	Thr	Pro	Gln	Tyr	Asp	Val	Ile	Ser	Thr	Glu
	35					40						45			
Pro	Val	Asn	Asn	His	Ile	Thr	Thr	Lys	Ala	Ile	Asn	Asn	Pro	Ala	Ser
	50					55					60				
Ser	Glu	Val	Thr	Ser	Thr	Val	Thr	Phe	Thr	Trp	Thr	Glu	Thr	Asp	Thr
	65					70				75					80
Val	Thr	Ser	Ala	Val	Thr	Lys	Gly	Tyr	Lys	Val	Gly	Gly	Ser	Val	Ser
						85			90					95	
Ser	Lys	Ala	Thr	Phe	Lys	Phe	Ala	Phe	Val	Thr	Ser	Asp	Val	Thr	Val
	100						105						110		
Thr	Val	Ser	Ala	Glu	Tyr	Asn	Tyr	Ser	Thr	Thr	Asp	Thr	Thr	Thr	Lys
	115						120					125			
Thr	Asp	Thr	Arg	Thr	Trp	Thr	Asp	Ser	Thr	Thr	Val	Lys	Ala	Pro	Pro
	130					135					140				
Arg	Thr	Asn	Val	Glu	Val	Ala	Tyr	Ile	Ile	Gln	Thr	Gly	Asn	Tyr	Asn
	145					150				155					160
Val	Pro	Val	Asn	Val	Glu	Ser	Asp	Met	Thr	Gly	Thr	Leu	Phe	Cys	Arg
						165				170				175	
Gly	Tyr	Arg	Asp	Gly	Ala	Leu	Ile	Ala	Ala	Thr	Tyr	Ile	Ser	Ile	Thr
						180			185				190		
Asp	Leu	Ala	Asp	Tyr	Lys	Pro	Asn	Leu	Gly	Leu	Thr	Asn	Lys	Gly	Asp
	195						200					205			
Gly	Val	Ala	His	Phe	Lys	Gly	Glu	Gly	Tyr	Ile	Glu	Gly	Ala	Gln	Gly
	210						215				220				
Leu	Arg	Ser	Tyr	Ile	Gln	Val	Thr	Glu	Tyr	Pro	Met	Asp	Asp	Lys	Asp
	225					230				235					240
Arg	Arg	Ser	Thr	Pro	Lys	Thr	Tyr	Thr	Ile	Glu	Gly	Ser	Leu	Ala	Pro
					245					250				255	
Asn	Val	Thr	Leu	Ile	Asn	Asp	Arg	Lys	Glu	Gly	Arg				
					260			265							

```
<210> SEQ ID NO 31
<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

```
<400> SEQUENCE: 31

atgggcatta tcaacattca agatgagatt aacgattaca tgaagggtat gtacggtgct 60
accagtgtga agtccacta cgatcctagt ttcaaggcttc tcaacgagtc tgtgactct 120
caatacgatg tgatttctac tgagcctgtg aacaatcaca ttactactaa ggctattaaac 180
aatccctgcta gttctgaggt tactagcact gttactttca ctggactga gactgatact 240
gttactagcg ctgttactaa gggttacaag gttggtgat ctgtttcttc aaaggctacc 300
ttcaagtttq ctttcgttac ctcaqatqt taccqttaccq tqaqcqctqa qtacaactac 360
```

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tcaaccacag ataccaccac caagaccgat accagaacct ggaccgattc aaccacagtg	420
aaggcaccac ctcgcaccaa cgtggaggtc gcctacatta tccaaacagg caactacaat	480
gtccccagtca atgtcgaatc cgacatgaca ggaacactct tctgccgtgg ctacaggat	540
ggagcactta ttgcagccac ctacatctcc atcacagacc ttgccgacta caagccaaat	600
cctcgactca caaacaaggg agacggcgtc gcccaactca aaggcgaagg ctacatcgaa	660
ggtgcccagg gtctaaggag ctacatccaa gtgacagaat acccaatgga cgacaaagac	720
cgtcgctcca caccaagac gtacaccatc gaagggtcgt taggccgaa tgtaacgctg	780
ataaatgacc gaaaggaagg gcggtga	807

<210> SEQ ID NO 32

<211> LENGTH: 268

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 32

Met Gly Ile Ile Asn Ile Gln Asp Glu Ile Asn Asp Tyr Met Lys Gly	
1 5 10 15	

Met Tyr Gly Ala Thr Ser Val Lys Ser Thr Tyr Asp Pro Ser Phe Lys	
20 25 30	

Val Phe Asn Glu Ser Val Thr Pro Gln Tyr Asp Val Ile Ser Thr Glu	
35 40 45	

Pro Val Asn Asn His Ile Thr Thr Lys Ala Ile Asn Asn Pro Ala Ser	
50 55 60	

Ser Glu Val Thr Ser Thr Val Thr Phe Thr Trp Thr Glu Thr Asp Thr	
65 70 75 80	

Val Thr Ser Ala Val Thr Lys Gly Tyr Lys Val Gly Gly Ser Val Ser	
85 90 95	

Ser Lys Ala Thr Phe Lys Phe Ala Phe Val Thr Ser Asp Val Thr Val	
100 105 110	

Thr Val Ser Ala Glu Tyr Asn Tyr Ser Thr Thr Asp Thr Thr Thr Lys	
115 120 125	

Thr Asp Thr Arg Thr Trp Thr Asp Ser Thr Thr Val Lys Ala Pro Pro	
130 135 140	

Arg Thr Asn Val Glu Val Ala Tyr Ile Ile Gln Thr Gly Asn Tyr Asn	
145 150 155 160	

Val Pro Val Asn Val Glu Ser Asp Met Thr Gly Thr Leu Phe Cys Arg	
165 170 175	

Gly Tyr Arg Asp Gly Ala Leu Ile Ala Ala Thr Tyr Ile Ser Ile Thr	
180 185 190	

Asp Leu Ala Asp Tyr Lys Pro Asn Leu Gly Leu Thr Asn Lys Gly Asp	
195 200 205	

Gly Val Ala His Phe Lys Gly Glu Gly Tyr Ile Glu Gly Ala Gln Gly	
210 215 220	

Leu Arg Ser Tyr Ile Gln Val Thr Glu Tyr Pro Met Asp Asp Lys Asp	
225 230 235 240	

Arg Arg Ser Thr Pro Lys Thr Tyr Thr Ile Glu Gly Ser Leu Ala Pro	
245 250 255	

Asn Val Thr Leu Ile Asn Asp Arg Lys Glu Gly Arg	
260 265	

<210> SEQ ID NO 33

-continued

<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis
<400> SEQUENCE: 33

```
atgacagtagtataaacgtaacctttaccattaaattctttaatcacggtaatgggggggg 60
ccagaaccttacggtaagatatatgcataatctcaaaaatcagatcataatttcgaaatt 120
tggtcacaagataattgggggaaggatacgcctgagaaaaatctcacac tcaaacaatt 180
aaaataagta gcccacagg gggcctata gaccaaatgt gtttatgg tgatgtaaaa 240
gaattcgcacg taggaaattc agatgatgtt ctcgcctctc caagtaaaa agtatgcagt 300
acgcctggca caacaataag gcttaacgga gatgagatgt gtttataat agagattgt 360
tattccttggccccagcttaa 381
```

<210> SEQ ID NO 34
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Bacillus thuringiensis
<400> SEQUENCE: 34

Met	Thr	Val	Tyr	Asn	Val	Thr	Phe	Thr	Ile	Lys	Phe	Phe	Asn	His	Gly
1															
															15
Glu	Trp	Gly	Pro	Glu	Pro	Tyr	Gly	Lys	Ile	Tyr	Ala	Tyr	Leu	Gln	
															30
Asn	Pro	Asp	His	Asn	Phe	Glu	Ile	Trp	Ser	Gln	Asp	Asn	Trp	Gly	Lys
															35
															40
															45
Asp	Thr	Pro	Glu	Lys	Ser	Ser	His	Thr	Gln	Thr	Ile	Lys	Ile	Ser	Ser
															50
															55
															60
Pro	Thr	Gly	Pro	Ile	Asp	Gln	Met	Cys	Phe	Tyr	Gly	Asp	Val	Lys	
															65
															70
															75
															80
Glu	Phe	Asp	Val	Gly	Asn	Ser	Asp	Asp	Val	Leu	Ala	Ser	Pro	Ser	Gln
															85
															90
															95
Lys	Val	Cys	Ser	Thr	Pro	Gly	Thr	Thr	Ile	Arg	Leu	Asn	Gly	Asp	Glu
															100
															105
															110
Ser	Gly	Ser	Tyr	Ile	Glu	Ile	Ser	Tyr	Ser	Leu	Ala	Pro	Ala		
															115
															120
															125

<210> SEQ ID NO 35
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 35

```
atgaccgtgtacaacgtgaccttcaccattaaagtcttcaatcacggtaatggggcggt 60
cctgagccatccatcgccatctccagaaccctgaccacaaatctcgaaatc 120
tggtcccaggacaactggggcaaggacactcccgagaatccagccatcgcacccatc 180
aagatcagca gccccactggcggcccgattgaccatgtgttctacggcgacgtcaag 240
gaatttgacgtggaaactcagatgacgtcctgccagccctgtccagaaatggggctcg 300
acgcaggaaatccatccgcctgaatggcgtgaatctggcgatcatcgacgtcgtatc 360
tacageccatcgccatcgatc 381
```

<210> SEQ ID NO 36
<211> LENGTH: 126

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 36

```

Met Thr Val Tyr Asn Val Thr Phe Thr Ile Lys Phe Phe Asn His Gly
1           5          10          15

Glu Trp Gly Gly Pro Glu Pro Tyr Gly Lys Ile Tyr Ala Tyr Leu Gln
20          25          30

Asn Pro Asp His Asn Phe Glu Ile Trp Ser Gln Asp Asn Trp Gly Lys
35          40          45

Asp Thr Pro Glu Lys Ser Ser His Thr Gln Thr Ile Lys Ile Ser Ser
50          55          60

Pro Thr Gly Gly Pro Ile Asp Gln Met Cys Phe Tyr Gly Asp Val Lys
65          70          75          80

Glu Phe Asp Val Gly Asn Ser Asp Asp Val Leu Ala Ser Pro Ser Gln
85          90          95

Lys Val Cys Ser Thr Pro Gly Thr Ile Arg Leu Asn Gly Asp Glu
100         105         110

Ser Gly Ser Tyr Ile Glu Ile Ser Tyr Ser Leu Ala Pro Ala
115         120         125

```

<210> SEQ ID NO 37
<211> LENGTH: 906
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis
<400> SEQUENCE: 37

```

atgaacaata attctaaatt tttattctca cctataatg ctaatggaaa taatccttat      60
tttttagatg tagataattg gaaagatgtt ttttgttac ttgtaaatc tctggaaatg     120
aaatatacaa aagttagttaa taaatctaa ttaatagatg cattattcc agatcctaatt    180
gatcaaagaa taggtccatt ttatttggaa atatatgata attataattt agataatgtt    240
ttaaaaccat tatatgattt tcatagttca ttatttggaa atattttgtt atggggatta   300
tttggacaa taagaatggg tagtttggtt tttcatattt aagatttgtt aaatatcata   360
tgtgtaaaac atataaatgtt attaatcaa attatagatg atttacaaca agataatgtt   420
tcaacaaaaa ctgttgataa atttagaaat atatgtattt aactacgtac taaatcactt   480
ctttttcctc aagaagttaa taaaatatta gatgcaaggta gaaatcttc aaataatctt   540
ataaaaagtta atgctatattt agattcaaca gtgcaacaat ttgaaaacgt ttatcaatca  600
tcacaatcaa ataacgataa atattatgg agaatcgtaa aagaatattt aggaaacgaa   660
caacaaagatt tagaaaaaca aactcctaat catcttaata ctcttcaaaa attacgtgga   720
atatggactg tttttggaga taattttagaa aaattaattt atgcttgc tttatcaatca  780
atagattttgc atgcaatgtt atgcttgc tttatcaatca 840
gaagttaaaaataatataga taaatttata ccagaatggg aaatctttaa aaaacaaggg   900
tgctaa                                         906

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<210> SEQ ID NO 38
<211> LENGTH: 301
<212> TYPE: PRT
<213> ORGANISM: Bacillus thuringiensis
<400> SEQUENCE: 38

-continued

Met Asn Asn Asn Ser Lys Phe Leu Phe Ser Pro Ile Asn Ala Asn Gly
 1 5 10 15
 Asn Asn Pro Tyr Phe Leu Asp Val Asp Asn Trp Lys Asp Val Phe Cys
 20 25 30
 Tyr Leu Val Asn Thr Leu Glu Met Lys Tyr Thr Lys Val Val Asn Lys
 35 40 45
 Ser Gln Leu Ile Asp Ala Leu Phe Pro Asp Pro Asn Asp Gln Arg Ile
 50 55 60
 Gly Pro Phe Tyr Trp Asn Ile Tyr Asp Asn Tyr Lys Leu Asp Asn Val
 65 70 75 80
 Leu Lys Pro Leu Tyr Asp Phe His Ser Ser Leu Leu Gly Asn Ile Leu
 85 90 95
 Glu Trp Gly Leu Phe Gly Thr Ile Arg Met Gly Ser Leu Ala Tyr His
 100 105 110
 Ile Gln Asp Phe Val Asn Ile Ile Cys Val Lys His Ile Asn Glu Phe
 115 120 125
 Asn Gln Ile Ile Asp Asp Leu Gln Asp Asn Val Ser Thr Lys Thr
 130 135 140
 Val Asp Lys Phe Arg Asn Ile Cys Ile Glu Leu Arg Thr Lys Ser Leu
 145 150 155 160
 Leu Phe Pro Gln Glu Val Asn Lys Ile Leu Asp Ala Ser Arg Asn Leu
 165 170 175
 Ala Asn Asn Leu Ile Lys Val Asn Ala Ile Leu Asp Ser Thr Val Gln
 180 185 190
 Gln Phe Glu Asn Val Tyr Gln Ser Ser Gln Ser Asn Asn Asp Lys Tyr
 195 200 205
 Tyr Leu Arg Ile Val Lys Glu Tyr Leu Gly Asn Glu Gln Gln Asp Leu
 210 215 220
 Glu Lys Gln Thr Pro Asn His Leu Asn Thr Leu Gln Lys Leu Arg Gly
 225 230 235 240
 Ile Trp Thr Val Phe Gly Asp Asn Leu Glu Lys Leu Ile His Ala Cys
 245 250 255
 Asp Asp Asp Leu Ile Asp Phe Asp Ala Met Ile Ala Ser Ile Asn Leu
 260 265 270
 Glu Asp Ala Ile Thr Ser Trp Lys Glu Val Lys Asn Asn Ile Asp Lys
 275 280 285
 Phe Ile Pro Glu Trp Glu Ile Phe Lys Lys Gln Gly Cys
 290 295 300

<210> SEQ ID NO 39
 <211> LENGTH: 906
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 39

```

atgaacaaca actctaagtt cctttctcg cccatcaacg ctaacggcaa caacccttac 60
ttccttagacg tggacaactg gaaggacgtc ttctgctacc tagtgaacac ccttgagatg 120
aagtacacta aggtggtaa caagtccag ctcattgacg ccctcttccc agatccta 180
gatcagcgta tcggaccctt ctactgaa acatcataactaagct cgacaacgtc 240
ctcaagccac tgtacgactt tcacagctca ctcctggca acatccttga gtggggactc 300
tttggacca ttcgcattgg ttctctggcc taccacatcc aagatttcgt caacattatc 360

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tgcgttaagc acatcaacga gttcaaccag	ataattgatg acctccagca agataacgtc	420
agcactaaga cgggtggacaa gttccgcac	atctgcacatcg aactccgcac gaagtccctt	480
ctgttccctc aggaggtaaa taagattctg	gatgcgtcac ggaacctcgc aaataacctc	540
atcaaggta atgcaatcct cgatagtagcc	gtccaacagt tcgagaacgt ttaccagtcg	600
tctcagtcta ataacgacaa gtactattt	agaatcgtaa aggagtatct cgggaatgag	660
cagcaagacc tggagaagca gacaccgaat	cacctgaaca cccttcagaa gctccgtggc	720
atctggacag tcttcggcga caatctttag	aagctcattc atgcttgta tgacgatctc	780
atcgacttcg acgctatgtat	cgcctccatc aacttggaaat gtcgtacac ttctgtggaa	840
gaggtaaga ataacattga caaattcatc	cctgaatggg aaatcttcaa gaaacaggc	900
tgctga		906

<210> SEQ_ID NO 40
<211> LENGTH: 301
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 40

Met Asn Asn Asn Ser Lys Phe Leu Phe Ser Pro Ile Asn Ala Asn Gly		
1 5 10 15		
Asn Asn Pro Tyr Phe Leu Asp Val Asn Trp Lys Asp Val Phe Cys		
20 25 30		
Tyr Leu Val Asn Thr Leu Glu Met Lys Tyr Thr Lys Val Val Asn Lys		
35 40 45		
Ser Gln Leu Ile Asp Ala Leu Phe Pro Asp Pro Asn Asp Gln Arg Ile		
50 55 60		
Gly Pro Phe Tyr Trp Asn Ile Tyr Asp Asn Tyr Lys Leu Asp Asn Val		
65 70 75 80		
Leu Lys Pro Leu Tyr Asp Phe His Ser Ser Leu Leu Gly Asn Ile Leu		
85 90 95		
Glu Trp Gly Leu Phe Gly Thr Ile Arg Met Gly Ser Leu Ala Tyr His		
100 105 110		
Ile Gln Asp Phe Val Asn Ile Ile Cys Val Lys His Ile Asn Glu Phe		
115 120 125		
Asn Gln Ile Ile Asp Asp Leu Gln Gln Asp Asn Val Ser Thr Lys Thr		
130 135 140		
Val Asp Lys Phe Arg Asn Ile Cys Ile Glu Leu Arg Thr Lys Ser Leu		
145 150 155 160		
Leu Phe Pro Gln Glu Val Asn Lys Ile Leu Asp Ala Ser Arg Asn Leu		
165 170 175		
Ala Asn Asn Leu Ile Lys Val Asn Ala Ile Leu Asp Ser Thr Val Gln		
180 185 190		
Gln Phe Glu Asn Val Tyr Gln Ser Ser Gln Ser Asn Asn Asp Lys Tyr		
195 200 205		
Tyr Leu Arg Ile Val Lys Glu Tyr Leu Gly Asn Glu Gln Gln Asp Leu		
210 215 220		
Glu Lys Gln Thr Pro Asn His Leu Asn Thr Leu Gln Lys Leu Arg Gly		
225 230 235 240		
Ile Trp Thr Val Phe Gly Asp Asn Leu Glu Lys Leu Ile His Ala Cys		
245 250 255		
Asp Asp Asp Leu Ile Asp Phe Asp Ala Met Ile Ala Ser Ile Asn Leu		

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260 265 270

Glu Asp Ala Ile Thr Ser Trp Lys Glu Val Lys Asn Asn Ile Asp Lys
 275 280 285

Phe Ile Pro Glu Trp Glu Ile Phe Lys Lys Gln Gly Cys
 290 295 300

<210> SEQ ID NO 41
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 41

atgaataata	ttaataagaa	gtatagactt	aatgatatga	ttaataaaaa	tcaatttatt	60
atttc当地	cagaatgggt	tactataaga	acatatattt	aaatttggatt	aactttacca	120
gttaatgaac	aagatttacg	aaaatatttc	aatttaatc	cagatataac	actatctat	180
gatTTTCTG	aatttatttga	tatttggtat	tctattaaaa	attttagctca	atggtggat	240
accactatac	tccctttaat	tattaaatct	gttaataata	ttacatcata	tggatttaaa	300
attgctggta	atccctttaa	taataaagaa	ggatactttt	caaaattaca	aatgaatta	360
catattattta	ataattataa	ttctaataaa	acaacaaaaa	ctattaaaca	atttcaatct	420
cgggtgtaca	ttttaattaa	ggaagttaaa	caatatgaag	atgttaccaa	aaatatttga	480
atattattaa	ataaaactttt	atatggtaat	cagcaaaaat	tagaagggt	tattaatatt	540
caaaaacgt	taaaagtgg	tcaaacaact	ttaatccga	tatctaatga	aactaattt	600
atttataaaa	aactatttga	aaaataaaaa	aaaataaata	ttggttttt	tgaatgcgt	660
aataaaatata	taagtatatt	taacaaaata	attattatgt	ggtcaaatac	tgaacaacaa	720
attatagatt	ttaaatcaat	tttatttca	gaattttaaa	atataaaatga	aacagttatt	780
gaatttgaag	atattatttga	gatttggta	attatagcta	aaaaatctcg	tgaatttact	840
ttaaatgctt	atatatctta	g				861

<210> SEQ ID NO 42
<211> LENGTH: 286
<212> TYPE: PRT
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 42

Met Asn Asn Ile Asn Lys	Lys Tyr Arg Leu Asn Asp	Met Ile Asn Lys	
1 5	10	15	
Asn Gln Phe Ile Ile Ser Lys	Thr Glu Trp Val Thr Ile Arg	Thr Tyr	
20	25	30	
Ile Glu Ile Gly Leu Thr Leu Pro Val Asn Glu Gln Asp	Leu Arg Lys		
35	40	45	
Tyr Phe Asn Leu Asn Pro Asp	Ile Thr Leu Ser Asn Asp	Phe Ser Glu	
50	55	60	
Leu Phe Asp Ile Cys Tyr Ser Ile Lys Asn	Leu Ala Gln Trp Trp Asn		
65	70	75	80
Thr Thr Ile Leu Pro Leu Ile Ile Lys	Ser Val Asn Asn Ile Thr Ser		
85	90	95	
Tyr Gly Phe Lys Ile Ala Gly Asn Pro Phe Asn Asn Lys	Glu Gly Tyr		
100	105	110	
Phe Ser Lys Leu Gln Asn Glu Leu His Ile Ile Asn Asn Tyr	Asn Ser		
115	120	125	
Asn Lys Thr Thr Lys Thr Ile Lys Gln Phe Gln Ser Arg	Cys Asn Ile		

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130	135	140
Leu Ile Lys Glu Val Lys Gln Tyr Glu Asp Val Thr Lys Asn Ile Val		
145	150	155
Ile Leu Leu Asn Lys Leu Leu Tyr Gly Asn Gln Gln Lys Leu Glu Gly		
165	170	175
Ile Ile Asn Ile Gln Lys Arg Leu Lys Val Val Gln Thr Thr Phe Asn		
180	185	190
Pro Ile Ser Asn Glu Thr Asn Leu Ile Tyr Lys Lys Leu Phe Glu Lys		
195	200	205
Ile Lys Lys Ile Asn Ile Gly Phe Phe Glu Cys Val Asn Lys Tyr Ile		
210	215	220
Ser Ile Phe Asn Lys Ile Ile Met Trp Ser Asn Thr Glu Gln Gln		
225	230	235
Ile Ile Asp Phe Lys Ser Ile Leu Phe Gln Glu Phe Lys Asn Ile Asn		
245	250	255
Glu Thr Val Ile Glu Phe Glu Asp Ile Ile Glu Ile Trp Leu Ile Ile		
260	265	270
Ala Lys Lys Ser Arg Glu Phe Thr Leu Asn Ala Tyr Ile Ser		
275	280	285

<210> SEQ ID NO 43
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 43

atgaacaaca ttaacaagaa gtaccgcctg aacgacatga ttaacaagaa ccagttcatc	60
attagcaaga ctgagtggtt gaccatcagg acgtacatcg agatcggtt gaccctggcc	120
gtgaacgagc aagacctgag gaagtacttc aacctaacc ctgacattac actgagcaac	180
gacttctcg agctgttgcg catctgtac tctatcaaga atctcgccca atgggtggaa	240
acaacgatcc ttccgctaat cattaagtct gtgaacaaca tcactagctt tggcttcaag	300
atcgcgggca acccggtcaa caataaggag ggttacttta gtaagtcacca gaacgaaactc	360
cacatcatta acaattacaa ttcaacaag acgactaaga cgatcaagca gtttcagtc	420
cggtgcaaca tcttgattaa ggagggtaaa caatacgaag atgttaacgaa gaacatcg	480
atcctccat acaaggtcct gtacggcaac cagcagaacg tcgaaggat cattaacata	540
cagaagcgtc tcaagggtgtt ccagaccacg ttcaatccc tctccaatga gactaacctt	600
atctacaaga aactcttga gaagatcaag aagatcaaca tcggcttctt tgagtgtgc	660
aacaagtaca tctccatctt caacaagata atcattatgt ggtcaaacac tgagcagcag	720
atcatcgact tcaagtccat actgttccag gagttcaaga acatcaatga gaccgtcatc	780
gagttcgaag acatcatcga gatttggctt atcatcgctt agaagtctag ggagttcacc	840
ctgaatgcgt acatctcctg a	861

<210> SEQ ID NO 44
<211> LENGTH: 286
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 44

-continued

Met Asn Asn Ile Asn Lys Lys Tyr Arg Leu Asn Asp Met Ile Asn Lys
 1 5 10 15
 Asn Gln Phe Ile Ile Ser Lys Thr Glu Trp Val Thr Ile Arg Thr Tyr
 20 25 30
 Ile Glu Ile Gly Leu Thr Leu Pro Val Asn Glu Gln Asp Leu Arg Lys
 35 40 45
 Tyr Phe Asn Leu Asn Pro Asp Ile Thr Leu Ser Asn Asp Phe Ser Glu
 50 55 60
 Leu Phe Asp Ile Cys Tyr Ser Ile Lys Asn Leu Ala Gln Trp Trp Asn
 65 70 75 80
 Thr Thr Ile Leu Pro Leu Ile Ile Lys Ser Val Asn Asn Ile Thr Ser
 85 90 95
 Tyr Gly Phe Lys Ile Ala Gly Asn Pro Phe Asn Asn Lys Glu Gly Tyr
 100 105 110
 Phe Ser Lys Leu Gln Asn Glu Leu His Ile Ile Asn Asn Tyr Asn Ser
 115 120 125
 Asn Lys Thr Thr Lys Thr Ile Lys Gln Phe Gln Ser Arg Cys Asn Ile
 130 135 140
 Leu Ile Lys Glu Val Lys Gln Tyr Glu Asp Val Thr Lys Asn Ile Val
 145 150 155 160
 Ile Leu Leu Asn Lys Leu Leu Tyr Gly Asn Gln Gln Lys Leu Glu Gly
 165 170 175
 Ile Ile Asn Ile Gln Lys Arg Leu Lys Val Val Gln Thr Thr Phe Asn
 180 185 190
 Pro Ile Ser Asn Glu Thr Asn Leu Ile Tyr Lys Lys Leu Phe Glu Lys
 195 200 205
 Ile Lys Lys Ile Asn Ile Gly Phe Glu Cys Val Asn Lys Tyr Ile
 210 215 220
 Ser Ile Phe Asn Lys Ile Ile Ile Met Trp Ser Asn Thr Glu Gln Gln
 225 230 235 240
 Ile Ile Asp Phe Lys Ser Ile Leu Phe Gln Glu Phe Lys Asn Ile Asn
 245 250 255
 Glu Thr Val Ile Glu Phe Glu Asp Ile Ile Glu Ile Trp Leu Ile Ile
 260 265 270
 Ala Lys Lys Ser Arg Glu Phe Thr Leu Asn Ala Tyr Ile Ser
 275 280 285

<210> SEQ_ID NO 45
 <211> LENGTH: 960
 <212> TYPE: DNA
 <213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 45

atgacaatta	caaataatcga	attagctata	cgagattata	caaattggga	tggtaactcgt	60
gaaattccgg	gatacatcaa	tcgtcagggtt	atagatgggc	caaataatata	tgactatgt	120
attagtgtact	ctgttagctgt	tccaaaaact	gtaattttca	atgtaaatcc	aactccatat	180
accggggcta	ataataatatc	agaaaataat	acagatgtaa	atcaaaataaa	acgttattaag	240
ttttctgaaa	aagtagttga	aactactaca	catactacta	caaagggttt	taaaattggc	300
gggttgaatta	aatctactac	aaaaggaact	ttaaaattaa	aatttcctgt	aggagaacta	360
gggtttgagc	aaactcttga	gctaccttct	acaggagaat	acaatagtag	ttccactacg	420
gggaacacctt	gtgcaaatga	aaaattatgg	gaaataacag	ataatataac	tgtacctcca	480
cattcacgtg	taacttcaac	ttaataatt	atgaaaacgg	aagtaagggt	tccaatggaa	540

ttaaccacta atcttagagg aactaattct agtggtaag gtcgttccc tactagtaat	600
ggtctttttt cataactac ttcagctcgt ggaactgttag gcggttattt tgtagttat	660
tacgtgaggc ctgcttctgc attgtataat acctcttggc ctgataaacc tgcaacttt	720
aattctattg gctcaaatga atctctaaat ttattggat ctggatattc tgacgtagtt	780
ccatctctat atgttactat tagacaagat caaaactccat tatcaggata tccaggtgaa	840
acgaaaacct ggtattcaga taaagtgata ttaagagatg gaagaattgt aacactacca	900
agcaatgctg atgtaaatat gtcacaaaca gccaaaattc catattgtga tagatctaa	960

<210> SEQ ID NO 46

<211> LENGTH: 319

<212> TYPE: PRT

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 46

Met Thr Ile Thr Asn Ile Glu Leu Ala Ile Arg Asp Tyr Thr Asn Trp			
1	5	10	15

Asp Gly Thr Arg Glu Ile Pro Gly Tyr Ile Asn Arg Gln Val Ile Asp			
20	25	30	

Gly Pro Asn Ile Tyr Asp Tyr Val Ile Ser Asp Ser Val Ala Val Pro			
35	40	45	

Lys Thr Val Ile Phe Asn Val Asn Pro Thr Pro Tyr Thr Gly Pro Asn			
50	55	60	

Ile Ile Ser Glu Asn Asn Thr Asp Val Asn Gln Asn Lys Arg Ile Lys			
65	70	75	80

Phe Ser Glu Lys Val Val Glu Thr Thr His Thr Thr Lys Gly			
85	90	95	

Phe Lys Ile Gly Gly Ile Lys Ser Thr Thr Lys Gly Thr Leu Lys			
100	105	110	

Leu Lys Phe Pro Val Gly Glu Leu Gly Phe Glu Gln Thr Leu Glu Leu			
115	120	125	

Pro Leu Thr Gly Glu Tyr Asn Ser Ser Ser Thr Thr Gly Asn Thr Cys			
130	135	140	

Ala Asn Glu Lys Leu Trp Glu Ile Thr Asp Asn Ile Thr Val Pro Pro			
145	150	155	160

His Ser Arg Val Thr Ser Thr Leu Ile Ile Met Lys Thr Glu Val Arg			
165	170	175	

Val Pro Met Glu Leu Thr Thr Asn Leu Arg Gly Thr Asn Ser Ser Gly			
180	185	190	

Glu Gly Ser Phe Pro Thr Ser Asn Gly Leu Phe Ser Tyr Thr Thr Ser			
195	200	205	

Ala Arg Gly Thr Val Gly Gly Ile Phe Val Ser Tyr Tyr Val Arg Pro			
210	215	220	

Ala Ser Ala Leu Tyr Asn Thr Ser Trp Pro Asp Lys Pro Ala Thr Phe			
225	230	235	240

Asn Ser Ile Gly Ser Asn Glu Ser Leu Asn Leu Leu Gly Ser Gly Tyr			
245	250	255	

Ser Asp Val Val Pro Ser Leu Tyr Val Thr Ile Arg Gln Asp Gln Thr			
260	265	270	

Pro Leu Ser Gly Tyr Pro Gly Glu Thr Lys Thr Trp Tyr Ser Asp Lys			
275	280	285	

Val Ile Leu Arg Asp Gly Arg Ile Val Thr Leu Pro Ser Asn Ala Asp			
290	295	300	

-continued

Val Asn Met Ser Gln Thr Ala Lys Ile Pro Tyr Cys Asp Arg Ser
 305 310 315

<210> SEQ ID NO 47
 <211> LENGTH: 960
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 47

atgaccatca ccaacatcga actcgccatc	cgcgactaca ctaactggga	cggcactagg	60
gagatccctg gctacatcaa ccgccaagtg	atcgacggcc cgaacatcta	cgactacgtg	120
atctctgact ccgtggccgt gcctaagacc	gtcatcttca acgtgaaccc	aactccgtac	180
actgggccaa acatcataaag cgagaacaat	actgacgtta atcagaacaa	gchgattaaag	240
ttctcggaga aggttgtgga gaccactacc	catacggacca caaaggcctt	caagatcggt	300
ggccggtatca agtccaccac gaaggggact	ctcaagctga aattccctgt	cggtgagctt	360
ggattttgagc aaaccctcga acttcctctg	acggggcgagt acaactccag	ctccaccact	420
gggaacacct ggcaccaacga gaaactgtgg	gaaatttaccc acaacataac	cgtcccccca	480
cactcccgag tcacctctac gcttatcatt	atgaagacag aagtaagggt	gccgatggag	540
ttgacgacta acctgcgtgg aacaaacagt	tccggcgaag ggagcttcc	tacctctaat	600
ggcctcttta gctacaccac atcagctaga	ggaaccgttg	gcccgtatctt	660
tacgtccgtc cggccagcgc actctacaac	acatcatggc	ctgacaagcc cgcgaccc	720
aatagcattg gtagcaatga gtcgctcaac	ctgctcggtt	ccgggttacag cgatgttg	780
cccaagctct atgttacgat cggcaagat	cagactccgc	tgtccggcta cccaggcgag	840
acaaagacat ggtactccga taaggtcatc	cttcgtatgg	ggcgcattgt caccctccct	900
tctaattgcgg atgtcaacat gagccagacg	gctaagatcc	cgtattgcga cccgtccctga	960

<210> SEQ ID NO 48
 <211> LENGTH: 319
 <212> TYPE: PRT
 <213> ORGANISM: Artificial sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 48

Met Thr Ile Thr Asn Ile Glu Leu Ala Ile Arg Asp Tyr	Thr Asn Trp	
1 5 10 15		
Asp Gly Thr Arg Glu Ile Pro Gly Tyr Ile Asn Arg Gln Val	Ile Asp	
20 25 30		
Gly Pro Asn Ile Tyr Asp Tyr Val Ile Ser Asp Ser Val	Ala Val Pro	
35 40 45		
Lys Thr Val Ile Phe Asn Val Asn Pro Thr Pro Tyr	Thr Gly Pro Asn	
50 55 60		
Ile Ile Ser Glu Asn Asn Thr Asp Val Asn Gln Asn Lys	Arg Ile Lys	
65 70 75 80		
Phe Ser Glu Lys Val Val Glu Thr Thr His Thr Thr Lys	Gly	
85 90 95		
Phe Lys Ile Gly Gly Ile Lys Ser Thr Thr Lys Gly Thr	Leu Lys	
100 105 110		
Leu Lys Phe Pro Val Gly Glu Leu Gly Phe Glu Gln Thr	Leu Glu Leu	
115 120 125		

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Pro Leu Thr Gly Glu Tyr Asn Ser Ser Ser Thr Thr Gly Asn Thr Cys
 130 135 140

Ala Asn Glu Lys Leu Trp Glu Ile Thr Asp Asn Ile Thr Val Pro Pro
 145 150 155 160

His Ser Arg Val Thr Ser Thr Leu Ile Ile Met Lys Thr Glu Val Arg
 165 170 175

Val Pro Met Glu Leu Thr Thr Asn Leu Arg Gly Thr Asn Ser Ser Gly
 180 185 190

Glu Gly Ser Phe Pro Thr Ser Asn Gly Leu Phe Ser Tyr Thr Thr Ser
 195 200 205

Ala Arg Gly Thr Val Gly Gly Ile Phe Val Ser Tyr Tyr Val Arg Pro
 210 215 220

Ala Ser Ala Leu Tyr Asn Thr Ser Trp Pro Asp Lys Pro Ala Thr Phe
 225 230 235 240

Asn Ser Ile Gly Ser Asn Glu Ser Leu Asn Leu Leu Gly Ser Gly Tyr
 245 250 255

Ser Asp Val Val Pro Ser Leu Tyr Thr Ile Arg Gln Asp Gln Thr
 260 265 270

Pro Leu Ser Gly Tyr Pro Gly Glu Thr Lys Thr Trp Tyr Ser Asp Lys
 275 280 285

Val Ile Leu Arg Asp Gly Arg Ile Val Thr Leu Pro Ser Asn Ala Asp
 290 295 300

Val Asn Met Ser Gln Thr Ala Lys Ile Pro Tyr Cys Asp Arg Ser
 305 310 315

<210> SEQ ID NO 49
 <211> LENGTH: 855
 <212> TYPE: DNA
 <213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 49

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atgaaaatatac acaaaaaatt tcatgaaata gcttggagtt tgctgaaaa atggactgaa 60
caagaaggttt tggaggtagc aaatgtcgat tatgtgaatct ctgctactgg taaagacacg 120
ttgaatttcg tgaataaattt tgaatatac ggaaaaataa aagaggaaaa tctttgc当地 180
gagatagtag caaatgagtc ttttcaat tcaaatgtg atactttgaa aaataatctc 240
cataaaaaat tattttgaa acaatattat ttatggata tagactatca atttataatt 300
ccgccttcaa ttatcacaaa tccaatatta ccgcctatgtc ttagaaaaa aatcaatcca 360
gcaatacagg tagattttt taaaagagca taccatgg aatctcaact aaacaattct 420
gaaataatag aagcaggat ttatattgaa cctaataaaa cgataaatgc taaagtaata 480
gcagaatata aaaaatgtgca acaaaaaat tttatcacacc taaaatttc aggaagtatt 540
gttatttgaaat ttgttatct tcgtatattct ttatggattt ctatccattt ttatctatc 600
ccaatcgtat atttgtataa atcagagctt gcacataatc attctttca tttatggatgg 660
gagactgtta tattttactga aaaaggatgtt tttaaaggcc taatggatc taatgtat 720
atcgaaaggaa aacgggtttaa tttaaaaaca ggagaatgtt taggttaata tataatacc 780
ttatggatgg acgaaagaaaa agttcttagaa aatagtaata caatatttt taattcagaa 840
aaaggaggaa tttaa

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<210> SEQ ID NO 50
 <211> LENGTH: 284
 <212> TYPE: PRT

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<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 50

Met	Lys	Tyr	His	Lys	Lys	Phe	His	Glu	Ile	Ala	Trp	Glu	Phe	Ala	Glu
1				5				10				15			

Lys	Trp	Thr	Glu	Gln	Glu	Gly	Leu	Glu	Leu	Ala	Asn	Val	Asp	Tyr	Val
		20				25						30			

Asn	Pro	Ala	Thr	Gly	Lys	Asp	Thr	Leu	Asn	Phe	Val	Asn	Lys	Phe	Glu
				35			40				45				

Tyr	Ile	Gly	Lys	Ile	Lys	Glu	Gly	Asn	Leu	Cys	Pro	Glu	Ile	Val	Ala
				50			55				60				

Asn	Glu	Ser	Phe	Ser	Asn	Ser	Lys	Cys	Asp	Thr	Leu	Lys	Asn	Asn	Leu
					65			70		75			80		

His	Lys	Lys	Leu	Phe	Leu	Lys	Gln	Tyr	Tyr	Leu	Trp	Asp	Ile	Asp	Tyr
				85				90				95			

Gln	Phe	Ile	Ile	Pro	Pro	Ser	Ile	Tyr	Thr	Asn	Pro	Ile	Leu	Pro	Pro
				100				105				110			

Cys	Leu	Ser	Lys	Lys	Ile	Asn	Pro	Ala	Ile	Gln	Val	Asp	Leu	Phe	Lys
					115			120			125				

Arg	Ala	Tyr	His	Phe	Glu	Ser	Gln	Leu	Asn	Asn	Ser	Glu	Ile	Ile	Glu
					130			135			140				

Ala	Gly	Ile	Tyr	Ile	Glu	Pro	Asn	Gln	Thr	Ile	Asn	Ala	Lys	Val	Ile
				145				150		155			160		

Ala	Glu	Tyr	Lys	Asn	Val	Gln	Gln	Lys	Tyr	Cys	Ile	His	Leu	Lys	Ile
					165			170			175				

Ser	Gly	Ser	Ile	Val	Ile	Glu	Val	Lys	Lys	Asn	Arg	Asn	Ser	Cys	Lys
					180			185			190				

Asp	Ser	Lys	Thr	Phe	Tyr	Thr	Ile	Pro	Ile	Val	Asp	Leu	Tyr	Lys	Ser
				195				200			205				

Glu	Leu	Ala	His	Asn	His	Ser	Phe	His	Leu	Asp	Gly	Glu	Thr	Val	Ile
					210			215			220				

Phe	Thr	Glu	Lys	Gly	Met	Phe	Lys	Gly	Leu	Ile	Cys	Ser	Asn	Val	Phe
					225			230		235			240		

Ile	Glu	Gly	Glu	Arg	Phe	Asn	Leu	Lys	Thr	Gly	Glu	Cys	Leu	Gly	Lys
					245			250			255				

Tyr	Ile	Ile	Pro	Leu	Gly	Met	Asp	Glu	Glu	Lys	Val	Leu	Glu	Asn	Ser
					260			265			270				

Lys	Ser	Ile	Ile	Phe	Phe	Asn	Ser	Glu	Lys	Gly	Gly	Ile		
					275			280						

<210> SEQ ID NO 51

<211> LENGTH: 855

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 51

atgaagtacc acaagaagtt ccacgagatc gcctgggagt tcgctgagaa gtggactgag 60

caggaggggcc tagagctggc taacgtggac tacgtgaacc ctgccacccg caaggacacc 120

ctgaacttcg tgaacaagtt cgagtacatc ggaaagatta aggagggaa cctctgtccc 180

gagattgttg ccaatgagtc tttcagcaat agcaagtgcg atacgtctaa gaataaaccc 240

cacaagaaac tgttcttcaa gcagttactac ctgtgggaca tcgactacca gttcatcatt 300

ccaccgagca tctacaccaa cccttatcctc cctccatgcc tgtcgaagaa gatcaacccg 360

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gccccatccaag tggacacctt caagcgcgct taccactttg agtcccagct taacaatagc	420
gagatcatcg aggccggtat ctacattgaa cccaaaccaga ccatcaatgc gaaggttatc	480
gcggaggtaca agaacgtgca acagaagtat tgcatccacc tcaagatcag tggtagtatt	540
gtcatcgagg tcaagaagaa caggaactcg tgcaaggact caaagacgtt ctacactatc	600
ccgatagtgg acctttacaa gtctgaactc gcccacaacc attcattcca tctcgatgga	660
gagactgtaa tcttcaccga gaaggccatg tttaaaggcc ttatggctc caacgtcttc	720
atcgaaggcg aacgcttcaa ccttaagaca ggagaatgcc tggggaaagta catcatccct	780
ttggggcatgg atgaggagaa gggttctggag aactccaagt ctatcttctt caactccgag	840
aaggggggga tctga	855

<210> SEQ ID NO 52

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 52

Met Lys Tyr His Lys Lys Phe His Glu Ile Ala Trp Glu Phe Ala Glu			
1	5	10	15

Lys Trp Thr Glu Gln Glu Gly Leu Glu Leu Ala Asn Val Asp Tyr Val			
20	25	30	

Asn Pro Ala Thr Gly Lys Asp Thr Leu Asn Phe Val Asn Lys Phe Glu			
35	40	45	

Tyr Ile Gly Lys Ile Lys Glu Gly Asn Leu Cys Pro Glu Ile Val Ala			
50	55	60	

Asn Glu Ser Phe Ser Asn Ser Lys Cys Asp Thr Leu Lys Asn Asn Leu			
65	70	75	80

His Lys Lys Leu Phe Leu Lys Gln Tyr Tyr Leu Trp Asp Ile Asp Tyr			
85	90	95	

Gln Phe Ile Ile Pro Pro Ser Ile Tyr Thr Asn Pro Ile Leu Pro Pro			
100	105	110	

Cys Leu Ser Lys Ile Asn Pro Ala Ile Gln Val Asp Leu Phe Lys			
115	120	125	

Arg Ala Tyr His Phe Glu Ser Gln Leu Asn Asn Ser Glu Ile Ile Glu			
130	135	140	

Ala Gly Ile Tyr Ile Glu Pro Asn Gln Thr Ile Asn Ala Lys Val Ile			
145	150	155	160

Ala Glu Tyr Lys Asn Val Gln Gln Lys Tyr Cys Ile His Leu Lys Ile			
165	170	175	

Ser Gly Ser Ile Val Ile Glu Val Lys Lys Asn Arg Asn Ser Cys Lys			
180	185	190	

Asp Ser Lys Thr Phe Tyr Thr Ile Pro Ile Val Asp Leu Tyr Lys Ser			
195	200	205	

Glu Leu Ala His Asn His Ser Phe His Leu Asp Gly Glu Thr Val Ile			
210	215	220	

Phe Thr Glu Lys Gly Met Phe Lys Gly Leu Ile Cys Ser Asn Val Phe			
225	230	235	240

Ile Glu Gly Glu Arg Phe Asn Leu Lys Thr Gly Glu Cys Leu Gly Lys			
245	250	255	

Tyr Ile Ile Pro Leu Gly Met Asp Glu Glu Lys Val Leu Glu Asn Ser			
260	265	270	

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Lys Ser Ile Phe Phe Asn Ser Glu Lys Gly Gly Ile
275 280

<210> SEQ ID NO 53
<211> LENGTH: 903
<212> TYPE: DNA
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 53

atgctagcat tcataatttc aggaggaagt agccaactt gtacgtcaat acgtaatgaa	60
tataataaca tattgcaagg gggggggatg gatgtatctt catccttccg tgttagatcct	120
tctaaaataa atataaatga tttggaagtg acatatccag agttaaatat tcccgataac	180
ataatagctt ctatagttatc taataatgc ttcgagaata gaggatttat aactaacgaa	240
acttacgcta ccgctgaggt aaccagagca ttaaccgaaa caattactac agctactact	300
agagggttta aattcacgca aggttttacc tatacaaata agattaacct cagaatacca	360
attgcgggtt cagaatcaac aatttcctt tcaacatctt ttgaacaaaaa tatttcaacc	420
actgaaacaa taacaaaaac tgaaacgata actatacttg tacctagaca aacggttaca	480
gtaaggccta gaacaagaaaa agttgttcaa ataagacttt atcaattacg aattcctaga	540
gtattcaccg aaatatctgc ttatgtaaca ggtactctt gacaaccaat tcctcaagcg	600
aatcctgatg tttatgctac tctggtaagt gtcaataatg catgtcctaa tgcatttgg	660
aaccgtgaca attttttag aatagatcgc gaaaagcggg gcttagcgtt aagaggagaa	720
ggtgaattta gtggaaatat agttcatta gatttcctga ttacgactac tgaatatgat	780
ttggatacaa atgctattat taatatacat aataccttg gcagagcagc tattctagga	840
agtgagcctt gtggaaactat tgcttataca gaaccaattt acattattca cactgatgt	900
taa	903

<210> SEQ ID NO 54
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 54

Met Leu Ala Phe Ile Phe Ser Gly Gly Ser Ser Gln Leu Cys Thr Ser	
1 5 10 15	
Ile Arg Asn Glu Tyr Asn Asn Ile Leu Gln Gly Gly Met Asp Val	
20 25 30	
Ser Ser Ser Phe Arg Val Asp Pro Ser Lys Ile Asn Ile Asn Asp Leu	
35 40 45	
Glu Val Thr Tyr Pro Glu Leu Asn Ile Pro Asp Asn Ile Ile Ala Ser	
50 55 60	
Ile Val Ser Asn Asn Ser Phe Glu Asn Arg Gly Phe Ile Thr Asn Glu	
65 70 75 80	
Thr Tyr Ala Thr Ala Glu Val Thr Arg Ala Leu Thr Glu Thr Ile Thr	
85 90 95	
Thr Ala Thr Thr Arg Gly Phe Lys Phe Thr Gln Gly Phe Thr Tyr Thr	
100 105 110	
Asn Lys Ile Asn Leu Arg Ile Pro Ile Ala Gly Ser Glu Ser Thr Ile	
115 120 125	
Ser Phe Ser Thr Ser Phe Glu Gln Asn Ile Ser Thr Thr Glu Thr Ile	
130 135 140	

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Thr Lys Thr Glu Thr Ile Thr Ile Leu Val Pro Arg Gln Thr Val Thr
 145 150 155 160
 Val Arg Pro Arg Thr Arg Lys Val Val Gln Ile Arg Leu Tyr Gln Leu
 165 170 175
 Arg Ile Pro Arg Val Phe Thr Glu Ile Ser Ala Tyr Val Thr Gly Thr
 180 185 190
 Leu Arg Gln Pro Ile Pro Gln Ala Asn Pro Asp Val Tyr Ala Thr Leu
 195 200 205
 Val Ser Val Asn Asn Ala Cys Pro Asn Ala Phe Val Asn Arg Asp Asn
 210 215 220
 Phe Leu Arg Ile Asp Arg Glu Lys Arg Gly Leu Ala Leu Arg Gly Glu
 225 230 235 240
 Gly Glu Phe Ser Gly Asn Ile Val Ser Leu Asp Phe Leu Ile Thr Thr
 245 250 255
 Thr Glu Tyr Asp Leu Asp Thr Asn Ala Ile Ile Asn Ile Asp Asn Thr
 260 265 270
 Leu Gly Arg Ala Ala Ile Leu Gly Ser Glu Pro Cys Gly Thr Ile Ala
 275 280 285
 Tyr Thr Glu Pro Ile Asp Ile Ile His Thr Asp Cys
 290 295 300

<210> SEQ ID NO 55

<211> LENGTH: 903

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 55

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atgccttgct tcatttctc cggcggttgc tcccagctct gcactagcat ccgtaacgag      60
tacaacaaca tcctccaggc cggtggcatg gacgtcagct ccagcttcgg cgtggaccct     120
agcaagatca acatcaacga ctttgagggtg acctatcctg agttgaacat tccagataac     180
attatcgcta gtattgttcc caacaacagt ttcgagaaca ggggattcat cactaacgag     240
acttacgcca cggccgaagt aacccgcgtt cttaactgaga cgattacgac tgccaccacg     300
cgccgattca agtttaccca ggggttcacc tacaccaaca agatcaacct ccgcattcca     360
atcgctggct ctgagttccac catctccttc tctacgtcg tgcgaacagaa catctcgacc     420
actgagacca tcacaaagac cgagactatac accatccttgc tgccaggca gaccgtcacc     480
gtcagacatcc ggaccaggaa ggtcggtcaa atccgttccat atcagttcg tattccgagg     540
gtgttcaccg agatttcagc gtatgttact ggcactctcc ggcageccat ccctcaagca     600
aacccggacg tttacgttac cttgtttcc gtcacacaatg cctggcccaa tgcttcgtg     660
aaccggacaca acttccttcg catcgaccgg gagaagcgcg gtctcgccgt gcgtggcgag     720
ggcgagttct ctggaaacat cgtctccctg gatttctgaa ttactacaac ggagtacgt     780
ctggatacaa acgctatcat caacattgac aacacgctcg ggcgcgcggc catacttggg     840
tcggaaacctt gcggtacaat agcatacaca gagcccatcg acatcattca cacagatgt     900
tga                                         903

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<210> SEQ ID NO 56

<211> LENGTH: 300

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 56

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Met Leu Ala Phe Ile Phe Ser Gly Gly Ser Ser Gln Leu Cys Thr Ser
1           5          10          15

Ile Arg Asn Glu Tyr Asn Asn Ile Leu Gln Gly Gly Gly Met Asp Val
20          25          30

Ser Ser Ser Phe Arg Val Asp Pro Ser Lys Ile Asn Ile Asn Asp Leu
35          40          45

Glu Val Thr Tyr Pro Glu Leu Asn Ile Pro Asp Asn Ile Ile Ala Ser
50          55          60

Ile Val Ser Asn Asn Ser Phe Glu Asn Arg Gly Phe Ile Thr Asn Glu
65          70          75          80

Thr Tyr Ala Thr Ala Glu Val Thr Arg Ala Leu Thr Glu Thr Ile Thr
85          90          95

Thr Ala Thr Thr Arg Gly Phe Lys Phe Thr Gln Gly Phe Thr Tyr Thr
100         105         110

Asn Lys Ile Asn Leu Arg Ile Pro Ile Ala Gly Ser Glu Ser Thr Ile
115         120         125

Ser Phe Ser Thr Ser Phe Glu Gln Asn Ile Ser Thr Thr Glu Thr Ile
130         135         140

Thr Lys Thr Glu Thr Ile Thr Ile Leu Val Pro Arg Gln Thr Val Thr
145         150         155         160

Val Arg Pro Arg Thr Arg Lys Val Val Gln Ile Arg Leu Tyr Gln Leu
165         170         175

Arg Ile Pro Arg Val Phe Thr Glu Ile Ser Ala Tyr Val Thr Gly Thr
180         185         190

Leu Arg Gln Pro Ile Pro Gln Ala Asn Pro Asp Val Tyr Ala Thr Leu
195         200         205

Val Ser Val Asn Asn Ala Cys Pro Asn Ala Phe Val Asn Arg Asp Asn
210         215         220

Phe Leu Arg Ile Asp Arg Glu Lys Arg Gly Leu Ala Leu Arg Gly Glu
225         230         235         240

Gly Glu Phe Ser Gly Asn Ile Val Ser Leu Asp Phe Leu Ile Thr Thr
245         250         255

Thr Glu Tyr Asp Leu Asp Thr Asn Ala Ile Ile Asn Ile Asp Asn Thr
260         265         270

Leu Gly Arg Ala Ala Ile Leu Gly Ser Glu Pro Cys Gly Thr Ile Ala
275         280         285

Tyr Thr Glu Pro Ile Asp Ile Ile His Thr Asp Cys
290         295         300

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<210> SEQ_ID NO 57

<211> LENGTH: 597

<212> TYPE: DNA

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 57

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atgaatacgt atcataaaat atgttctggc ctttatcagt ataattcacaa aggtccctac      60
acggaatgtg ggcctactcc taggagatcc aatcccgtat aagaacatcc aactttaaaa     120
gattcatacg gtgatcctgt cctcttattac atgccctatt atatggatcc atatgaattt    180
cctggtaaaa gatttgttgc cgaatggact tctgtggatc atcgtggatc taaatttagga    240
acgtctttag cgaaagttt tttgcacttt tgaaaaagcta atggttccga tagtgcttta    300
cgtatcaata tattggatcg tgaggaaac ccagaaaatc agtacttatac taagaaacgt    360

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ggtaactgacg aagtacttatt atataatcat gaccctctag aatccgaatg ggttccggag	420
aattcatctg atcctaattt ttcaatgttca aactacttct cactccaaa tgcttcggat	480
catattatcc ccaatgaaaa attcttatcc tatagcattc caggtgaatg gttaaccaca	540
gttcagccatc ctatgaattc aaaaacaatg tggcgtttaa ttccaacatg gaaataa	597

<210> SEQ ID NO 58

<211> LENGTH: 198

<212> TYPE: PRT

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 58

Met Asn Thr Tyr His Lys Ile Cys Ser Gly Pro Tyr Gln Tyr Asn His	
1 5 10 15	

Lys Gly Pro Tyr Thr Glu Cys Gly Pro Thr Pro Arg Arg Ser Asn Pro	
20 25 30	

Asp Glu Glu His Ser Thr Leu Lys Asp Ser Tyr Gly Asp Pro Val Leu	
35 40 45	

Tyr Tyr Met Pro Tyr Tyr Met Asp Pro Tyr Glu Phe Pro Gly Glu Arg	
50 55 60	

Phe Val Tyr Glu Trp Thr Ser Asp Gly Asp Arg Gly Val Lys Leu Gly	
65 70 75 80	

Thr Ser Tyr Ala Lys Val Tyr Leu His Phe Trp Lys Ala Asn Gly Ser	
85 90 95	

Asp Ser Ala Leu Arg Ile Asn Ile Leu Asp Arg Glu Gly Asn Pro Glu	
100 105 110	

Asn Gln Tyr Leu Ser Lys Lys Arg Gly Thr Asp Glu Val Leu Leu Tyr	
115 120 125	

Asn His Asp Pro Leu Glu Ser Glu Trp Val Pro Glu Asn Ser Ser Asp	
130 135 140	

Pro Asn Phe Ser Val Gly Asn Tyr Phe Ser Leu Gln Asn Ala Ser Asp	
145 150 155 160	

His Ile Ile Ser Asn Glu Lys Phe Leu Ser Tyr Ser Ile Pro Gly Glu	
165 170 175	

Trp Leu Thr Thr Val Gln Pro Thr Met Asn Ser Lys Thr Met Trp Arg	
180 185 190	

Leu Ile Pro Thr Trp Lys	
195	

<210> SEQ ID NO 59

<211> LENGTH: 660

<212> TYPE: DNA

<213> ORGANISM: *Bacillus thuringiensis*

<400> SEQUENCE: 59

atgaatacgc atcataaaat gtgttctagt ctttatcgat ataatcatag acataaggat	60
---	----

tgcgattgtc atttatataa ccataacggt ctttatcgat ataatcacag aggtccctac	120
---	-----

acgaaatgtg gacctactcc taggatca aatcccgtatc aagaacatcc aactttaaa	180
---	-----

gattcatacg gtgatccagt ccgctatagc atgccctatt atatggatcc atatgaattt	240
---	-----

cctggtaaaa gatttgttca cgaatggact tctgatggag atcgtggagt taaatttaga	300
---	-----

acgtctttagt cgagtgttta tttgtacttt tggaaaatta ataatggatc cgatgtgct	360
---	-----

ttacgtatca atatatttggaa tcgtgaggaa aacccagaaa atcagtactt atctaagaaa	420
---	-----

cgtggtaactg acgaagttactt attatataat cgtgaccctc tagaatccga atgggttccg	480
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gagaattcat ctgatcctaa ttttcagta ggaaactact tctcaactcca aagtgcgtcg	540
gatcatatta ttccaatga aaaattctta tcctatagca ttcccggtga atggtaacc	600
acagttcagc ctactatgaa ttcaaaaaca atgtggcggt taattccagc atggaaataa	660

<210> SEQ ID NO 60

<211> LENGTH: 219

<212> TYPE: PRT

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 60

Met Asn Thr His His Lys Met Cys Ser Ser Pro Tyr Arg Tyr Asn His	
1 5 10 15	

Arg His Lys Asp Cys Asp Cys His Leu Tyr Asn His Asn Gly Pro Tyr	
20 25 30	

Gln Tyr Asn His Arg Gly Pro Tyr Thr Glu Cys Gly Pro Thr Pro Arg	
35 40 45	

Arg Ser Asn Pro Asp Glu Glu His Ser Thr Leu Lys Asp Ser Tyr Gly	
50 55 60	

Asp Pro Val Arg Tyr Ser Met Pro Tyr Tyr Met Asp Pro Tyr Glu Phe	
65 70 75 80	

Pro Gly Glu Arg Phe Val Tyr Glu Trp Thr Ser Asp Gly Asp Arg Gly	
85 90 95	

Val Lys Leu Gly Thr Ser Tyr Ala Ser Val Tyr Leu Tyr Phe Trp Lys	
100 105 110	

Ile Asn Asn Gly Thr Asp Ser Ala Leu Arg Ile Asn Ile Leu Asp Arg	
115 120 125	

Glu Gly Asn Pro Glu Asn Gln Tyr Leu Ser Lys Lys Arg Gly Thr Asp	
130 135 140	

Glu Val Leu Leu Tyr Asn Arg Asp Pro Leu Glu Ser Glu Trp Val Pro	
145 150 155 160	

Glu Asn Ser Ser Asp Pro Asn Phe Ser Val Gly Asn Tyr Phe Ser Leu	
165 170 175	

Gln Ser Ala Ser Asp His Ile Ile Ser Asn Glu Lys Phe Leu Ser Tyr	
180 185 190	

Ser Ile Pro Gly Glu Trp Leu Thr Thr Val Gln Pro Thr Met Asn Ser	
195 200 205	

Lys Thr Met Trp Arg Leu Ile Pro Ala Trp Lys	
210 215	

<210> SEQ ID NO 61

<211> LENGTH: 597

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 61

atgaacacct accacaagat ttgctccggc ctttaccagt acaaccacaa gggaccgtac	60
---	----

actgagtgcg gccctacccc taggcgtacg aaccctgacg aggagcac tcacccttaag	120
--	-----

gactcctacg gtgacccagt gctctactac atgccgtact acatggaccc atacgaggtc	180
---	-----

cctggcgaaa gttcgtgtc cgagtgacg tcagatggac atagaggagt caagctcggt	240
---	-----

actagctatg cgaaagttt cctacactc tggaggcta acgggtctga ctccgccttg	300
--	-----

cggtcaaca ttctcgatag ggaggcaac cctgagaacc agtatctctc caagaagcgc	360
---	-----

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ggcacccatg aggttcttct	gtacaaccac	gacccacttg	agtccgaatg	ggttccagaa	420
aacagctcg acccgaactt	cagegtggaa	aactactca	gtctccagaa	cgcacatcgat	480
cacatcatct cgaatgagaa	gttctctct	tattctatcc	caggcgagtg	gctgactacc	540
gtgcaaccta cgatgaatag	taagacaatg	tggaggctca	ttccgacatg	gaagtga	597

<210> SEQ ID NO 62
<211> LENGTH: 198
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 62

Met Asn Thr Tyr His Lys Ile Cys Ser Gly Pro Tyr Gln Tyr Asn His					
1	5	10	15		

Lys Gly Pro Tyr Thr Glu Cys Gly Pro Thr Pro Arg Arg Ser Asn Pro					
20	25	30			

Asp Glu Glu His Ser Thr Leu Lys Asp Ser Tyr Gly Asp Pro Val Leu					
35	40	45			

Tyr Tyr Met Pro Tyr Tyr Met Asp Pro Tyr Glu Phe Pro Gly Glu Arg					
50	55	60			

Phe Val Tyr Glu Trp Thr Ser Asp Gly Asp Arg Gly Val Lys Leu Gly					
65	70	75	80		

Thr Ser Tyr Ala Lys Val Tyr Leu His Phe Trp Lys Ala Asn Gly Ser					
85	90	95			

Asp Ser Ala Leu Arg Ile Asn Ile Leu Asp Arg Glu Gly Asn Pro Glu					
100	105	110			

Asn Gln Tyr Leu Ser Lys Lys Arg Gly Thr Asp Glu Val Leu Leu Tyr					
115	120	125			

Asn His Asp Pro Leu Glu Ser Glu Trp Val Pro Glu Asn Ser Ser Asp					
130	135	140			

Pro Asn Phe Ser Val Gly Asn Tyr Phe Ser Leu Gln Asn Ala Ser Asp					
145	150	155	160		

His Ile Ile Ser Asn Glu Lys Phe Leu Ser Tyr Ser Ile Pro Gly Glu					
165	170	175			

Trp Leu Thr Thr Val Gln Pro Thr Met Asn Ser Lys Thr Met Trp Arg					
180	185	190			

Leu Ile Pro Thr Trp Lys					
195					

<210> SEQ ID NO 63
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 63

atgaacaccc accacaagat	gtgctctagc	ccttaccgct	acaaccaccc	ccacaaggac	60
tgcgactgcc	acctctacaa	ccacaacgga	ccctaccagt	acaaccatag	120
actgagtgtg	gccctactcc	taggcgtgc	aaccggacg	aggaacacag	180
gactcctacg	gcgaccctgt	gagatactcc	atgccttact	acatggaccc	240
ccaggcgacg	gcttcgtgta	cgagtggacc	tccgacggcg	acagaggtgt	300
acctcctacg	cctccgtgta	cctctacttc	tggaagatca	acaatggtac	360

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cttcggatca acatcctgga tagggagggc aacccggaga accagtatct gagcaagaaa	420
cgcggcactg atgagggtgct gcttacaac cgtgatccgc tggagagcga gtgggtgccg	480
gagaactctt cggaccctaa cttagtgcgtt ggaaattact tcagttcca gtcagcgta	540
gatcacatca tctctaataa gaagttccctg tcctactcga tcccaggaga atggctcagc	600
acagttcaac ccacgatgaa ctcgaagaca atgtggcgat tgataccagc atggaaatga	660

<210> SEQ ID NO 64

<211> LENGTH: 219

<212> TYPE: PRT

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: an amino acid sequence translation of SEQ ID NO: 63.

<400> SEQUENCE: 64

Met Asn Thr His His Lys Met Cys Ser Ser Pro Tyr Arg Tyr Asn His	
1 5 10 15	

Arg His Lys Asp Cys Asp Cys His Leu Tyr Asn His Asn Gly Pro Tyr	
20 25 30	

Gln Tyr Asn His Arg Gly Pro Tyr Thr Glu Cys Gly Pro Thr Pro Arg	
35 40 45	

Arg Ser Asn Pro Asp Glu Glu His Ser Thr Leu Lys Asp Ser Tyr Gly	
50 55 60	

Asp Pro Val Arg Tyr Ser Met Pro Tyr Tyr Met Asp Pro Tyr Glu Phe	
65 70 75 80	

Pro Gly Glu Arg Phe Val Tyr Glu Trp Thr Ser Asp Gly Asp Arg Gly	
85 90 95	

Val Lys Leu Gly Thr Ser Tyr Ala Ser Val Tyr Leu Tyr Phe Trp Lys	
100 105 110	

Ile Asn Asn Gly Thr Asp Ser Ala Leu Arg Ile Asn Ile Leu Asp Arg	
115 120 125	

Glu Gly Asn Pro Glu Asn Gln Tyr Leu Ser Lys Lys Arg Gly Thr Asp	
130 135 140	

Glu Val Leu Leu Tyr Asn Arg Asp Pro Leu Glu Ser Glu Trp Val Pro	
145 150 155 160	

Glu Asn Ser Ser Asp Pro Asn Phe Ser Val Gly Asn Tyr Phe Ser Leu	
165 170 175	

Gln Ser Ala Ser Asp His Ile Ile Ser Asn Glu Lys Phe Leu Ser Tyr	
180 185 190	

Ser Ile Pro Gly Glu Trp Leu Thr Thr Val Gln Pro Thr Met Asn Ser	
195 200 205	

Lys Thr Met Trp Arg Leu Ile Pro Ala Trp Lys	
210 215	

What is claimed is:

1. A DNA construct comprising a polynucleotide operably linked to a heterologous promoter, wherein said polynucleotide encodes a pesticidal polypeptide that comprises the amino acid sequence as set forth in SEQ ID NO:50.

2. The DNA construct of claim 1, wherein said polynucleotide is codon-optimized for expression in a plant.

3. The DNA construct of claim 2, wherein said polynucleotide comprises the nucleic acid sequence as set forth in SEQ ID NO:51.

4. A host cell comprising a DNA construct that comprises a polynucleotide operably linked to a heterologous promoter,

55 wherein said polynucleotide encodes a pesticidal polypeptide that comprises the amino acid sequence as set forth in SEQ ID NO:50.

5. The host cell of claim 4, wherein said host cell is a bacterial cell or a plant cell.

60 6. The host cell of claim 5, wherein said bacterial cell is selected from the group consisting of an *Agrobacterium*, a *Bacillus*, an *Escherichia*, a *Salmonella*, a *Pseudomonas*, and a *Rhizobium* cell, and wherein said plant cell is selected from the group consisting of a alfalfa, banana, barley, bean, broccoli, cabbage, canola, carrot, cassava, castor, cauliflower, celery, chickpea, Chinese cabbage, citrus, coconut, coffee, corn, clover, cotton, a cucurbit, cucumber, Douglas fir, eggplant,

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eucalyptus, flax, garlic, grape, hops, leek, lettuce, Loblolly pine, millets, melons, nut, oat, olive, onion, ornamental, palm, pasture grass, pea, peanut, pepper, pigeonpea, pine, potato, poplar, pumpkin, Radiata pine, radish, rapeseed, rice, rootstocks, rye, safflower, shrub, sorghum, Southern pine, soybean, spinach, squash, strawberry, sugar beet, sugarcane, sunflower, sweet corn, sweet gum, sweet potato, switchgrass, tea, tobacco, tomato, triticale, turf grass, watermelon, and a wheat plant cell.

7. A plant, or part thereof, comprising a polynucleotide encoding a pesticidal polypeptide that comprises the amino acid sequence as set forth in SEQ ID NO:50.

8. The plant, or part thereof, of claim 7, wherein said plant is elected from the group consisting of a alfalfa, banana, barley, bean, broccoli, cabbage, canola, carrot, cassava, castor, cauliflower, celery, chickpea, Chinese cabbage, citrus, coconut, coffee, corn, clover, cotton, a cucurbit, cucumber, Douglas fir, eggplant, eucalyptus, flax, garlic, grape, hops, leek, lettuce, Loblolly pine, millets, melons, nut, oat, olive, onion, ornamental, palm, pasture grass, pea, peanut, pepper, pigeonpea, pine, potato, poplar, pumpkin, Radiata pine, radish, rapeseed, rice, rootstocks, rye, safflower, shrub, sorghum, Southern pine, soybean, spinach, squash, strawberry, sugar beet, sugarcane, sunflower, sweet corn, sweet gum, sweet potato, switchgrass, tea, tobacco, tomato, triticale, turf grass, watermelon, and a wheat plant, and wherein said part is selected from the group consisting of a leaf, a stem a flower, a sepal, a fruit, a root, or a seed.

9. A method of controlling a pest infection of a plant, said method comprising providing in a diet of said pest a plant, or part thereof, said plant or part comprising a polynucleotide encoding a pesticidal polypeptide that comprises the amino acid sequence as set forth in SEQ ID NO:50.

10. The method of claim 9, wherein said pest is an insect or a nematode.

11. The method of claim 10, wherein said insect is an insect from the insect order selected from the group consisting of Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthoptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, and Trichoptera, and wherein said nematode is selected from the group consisting of *Acontylus*, *Anguina*, *Aorolaimus*, *Aphasmatylenchus*, *Aphelenchooides*, *Aphelenchus*, *Atalodera*, *Aty-*

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lenchus, *Bakernema*, *Belonolaimus*, *Brachyedorus*, *Bursaphelenchus*, *Cacopaurus*, *Caloosia*, *Carpodorus*, *Criconema*, *Criconemella*, *Cryphodera*, *Ditylenchus*, *Dolichodorus*, *Eutylechus*, *Globodera*, *Gracilacus*, *Helicotylenchus*, *Hemicriconemoides*, *Hemicyclophora*, *Heterodera*, *Hirschmanniella*, *Histotylenchus*, *Hoplolaimus*, *Hoplotyulus*, *Longidorus*, *Macrotyphurus*, *Meloidodera*, *Meloidogyne*, *Merlinius*, *Morulaimus*, *Nacobbus*, *Nothanguina*, *Nothotylenchus*, *Paralongidorus*, *Paratrichodorus*, *Paratrophurus*, *Paratylenchus*, *Peltamigratus*, *Pratylenchooides*, *Pratylenchus*, *Psilenchus*, *Radopholoides*, *Radopholus*, *Rhadinaphelenchus*, *Rototylenchus*, *Rotylenchooides*, *Rotylenchus*, *Sarisodera*, *Scutellonema*, *Sphaeronema*, *Subanguina*, *Telotylenchooides*, *Telotylenchus*, *Trichotylenchus*, *Trophonema*, *Trophotylenclus*, *Trophurus*, *Tylenchorhynchus*, *Tylenchulus*, *Tylenchus*, *Tyloadorus*, *Xiphinema*, and *Zygotylenchus* nematode.

12. The method of claim 9, said method further comprising providing in the diet of said pest a pesticidally effective amount of one or more other toxic agents selected from the group consisting of methylketone synthase, a Cry protein, a VIP protein, and a chemical nematicide.

13. The method of claim 9, said method further comprising providing in a diet of said pest a pesticidally effective amount of one or more pesticidal polypeptides, wherein said one or more pesticidal polypeptides comprise SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO:26, SEQ ID NO:30, SEQ ID NO:34, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:46, SEQ ID NO:54, SEQ ID NO:58, or SEQ ID NO:60, or a pesticidal fragment thereof.

14. The method of claim 13, wherein the pesticidally effective amount of said one or more pesticidal polypeptides is provided by the plant, which is a recombinant plant, a part of the plant, or a product of the plant or the plant part.

15. The method of claim 13, wherein the pesticidally effective amount of said one or more pesticidal polypeptides is provided in one or more formulations topically applied on the plant or a part of the plant, said one or more formulations comprising bacterial cells, spores, or parasporal crystals that comprise said one or more pesticidal polypeptides.

* * * * *